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OM protein - protein search, using sw model

Run on: March 26, 2003, 09:54:07 ; Search time 28 Seconds  
(without alignments)  
334,160 Million cell updates/sec

File: US-09-966-459a-2

Perfect score: 1623

Sequence: 1 MWDPNNGESSATFILLGL.....KEIKRIILFLFVAFHASEP 318

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: \*  
1: /cgcn2\_6/ptodata/1/1aa/5A\_COMB.pep: \*  
2: /cgcn2\_6/ptodata/1/1aa/5B\_COMB.pep: \*  
3: /cgcn2\_6/ptodata/1/1aa/5A\_COMB.pep: \*  
4: /cgcn2\_6/ptodata/1/1aa/5B\_COMB.pep: \*  
5: /cgcn2\_6/ptodata/1/1aa/5A\_COMB.pep: \*  
6: /cgcn2\_6/ptodata/1/1aa/5B\_COMB.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	983	60.6	320	4	US-09-605-785-527
2	983	60.6	320	4	US-09-605-785-527
3	968.5	59.7	320	1	US-08-465-980-2
4	968.5	59.7	320	2	US-09-053-303-2
5	968.5	59.7	320	4	US-09-339-115-2
6	968.5	59.7	320	4	US-09-339-115-2
7	968.5	59.7	320	4	US-09-339-115-2
8	968.5	59.7	320	4	US-09-339-115-2
9	968.5	59.7	320	4	US-09-339-115-2
10	968.5	59.7	320	4	US-09-339-115-2
11	968.5	59.7	320	4	US-09-339-115-2
12	968.5	59.7	320	4	US-09-339-115-2
13	968.5	59.7	320	4	US-09-339-115-2
14	968.5	59.7	320	4	US-09-339-115-2
15	968.5	59.7	320	4	US-09-339-115-2
16	968.5	59.7	320	4	US-09-339-115-2
17	968.5	59.7	320	4	US-09-339-115-2
18	968.5	59.7	320	4	US-09-339-115-2
19	968.5	59.7	320	4	US-09-339-115-2
20	968.5	59.7	320	4	US-09-339-115-2
21	968.5	59.7	320	4	US-09-339-115-2
22	968.5	59.7	320	4	US-09-339-115-2
23	968.5	59.7	320	4	US-09-339-115-2
24	968.5	59.7	320	4	US-09-339-115-2
25	968.5	59.7	320	4	US-09-339-115-2
26	968.5	59.7	320	4	US-09-339-115-2
27	968.5	59.7	320	4	US-09-339-115-2

28	336.5	20.7	293	1	US-08-118-270-60	Sequence 60, Appl
29	336.5	20.7	293	5	PCT-US93-08528-60	Sequence 60, Appl
30	335.5	20.7	277	1	US-08-118-270-62	Sequence 62, Appl
31	335.5	20.7	277	5	PCT-US93-08528-62	Sequence 62, Appl
32	333.5	20.5	321	4	US-08-748-506-11	Sequence 11, Appl
33	332.5	20.5	327	4	US-08-748-506-22	Sequence 22, Appl
34	332.5	20.5	327	4	US-08-748-506-22	Sequence 22, Appl
35	330	20.3	321	4	US-08-748-506-19	Sequence 19, Appl
36	329	20.3	277	1	US-08-118-270-68	Sequence 68, Appl
37	329	20.3	277	5	PCT-US93-08528-68	Sequence 68, Appl
38	326	20.1	286	5	US-08-118-270-65	Sequence 65, Appl
39	326	20.1	286	5	PCT-US93-08528-65	Sequence 65, Appl
40	320	19.7	274	1	US-08-118-270-69	Sequence 69, Appl
41	320	19.7	274	5	PCT-US93-08528-69	Sequence 69, Appl
42	318.5	19.6	275	1	US-08-118-270-66	Sequence 66, Appl
43	318.5	19.6	275	5	PCT-US93-08528-66	Sequence 66, Appl
44	318	19.6	273	1	US-08-118-270-63	Sequence 63, Appl
45	318	19.6	273	5	PCT-US93-08528-63	Sequence 63, Appl

#### ALIGNMENTS

RESULT 1	
US-09-605-785-527	
Sequence 527, Application US/09605785	
Patent No. 6321716	
GENERAL INFORMATION:	
APPLICANT: Xu, Jiangchun	
APPLICANT: Dillion, Davin C.	
APPLICANT: Matchem, Jennifer L.	
APPLICANT: Harlocker, Susan L.	
APPLICANT: Jiang, Yugu	
APPLICANT: Henderson, Robert A.	
APPLICANT: Kalos, Michael D.	
APPLICANT: Fanger, Gary R.	
APPLICANT: Reiter, Marc W.	
APPLICANT: Stolk, John A.	
APPLICANT: Day, Craig H.	
APPLICANT: Vedvick, Thomas S.	
APPLICANT: Carter, Darrick	
APPLICANT: Li, Samuel	
APPLICANT: Wang, Aijun	
APPLICANT: Skeiky, Yasir A.W.	
APPLICANT: Hepler, William	
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	
FILE REFERENCE: 210121.427C16	
CURRENT APPLICATION NUMBER: US/09/605,785	
CURRENT FILING DATE: 2000-06-27	
NUMBER OF SEQ ID NOS: 835	
SOFTWARE: FASTSEQ for Windows Version 3.0	
SEQ ID NO 527	
LENGTH: 320	
TYPE: PRT	
ORGANISM: Homo sapiens	
US-09-605-785-527	
Query Match	
Best Local Similarity 59.8%; Score 983; DB 4; Length 320;	
Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;	
QY	8 NESAATFILLIGLPGLEAOFMLAFLPCSLYLAVLNTIIVYREHSIHPEMTFLC 67
DB	5 NHTAT FVILIGLPGLEAOFMLAFLPCSLYLAVLNTIIVYREHSIHPEMTFLC 63
QY	68 MSLGIDILISTSPMKALAFNFTSTTOPDACLONFAHSLSGMSSTVLAARDRY 127
DB	64 MSLGIDILISTSPMKALAFNFTSTTOPDACLONFAHSLSGMSSTVLAARDRY 123
QY	128 AICHPRLRAHVLLPRTKRGVAAVYRGALAPLPVFIKOLPFGSNITSHYCIADY 187
DB	124 AICHPRLRAHVLLPRTKRGVAAVYRGALAPLPVFIKOLPFGSNITSHYCIADY 183





;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,  
;; ADDRESSEE: STUART & OLSTEIN  
;; STREET: 6 Becker Farm Road  
;; CITY: Roseland  
;; STATE: New Jersey  
;; COUNTRY: USA  
;; ZIP: 07068  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: PCT/US95/07093  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/465,980  
;; FILING DATE: 06-JUN-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Ferraro, Gregory D.  
;; REGISTRATION NUMBER: 36,134  
;; REFERENCE/DOCKET NUMBER: 325800-446  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 201-994-1700  
;; TELEFAX: 201-994-1744  
;; INFORMATION FOR SEQ ID NO: 2:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 320 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; PCT-US95-07093-2

Query Match 59.7%; Score 968.5; DB 5; Length 320;  
Best Local Similarity 59.7%; Pred. No. 1.9e-81;  
Matches 178; Conservative 53; Mismatches 66; Indels 1; Gaps 1;

DB 12 VILGIGLEAOWFLAFPLCSLYLNAVGNLTIIYVREHSHHEPMYIFLCMSGIDIL 75  
QY 16 IILGIGLEAOWFLAFPLCSLYLNAVGNLTIIYVREHSHHEPMYIFLCMSGIDIL 75  
DB 76 IISTSPKMLATFWNSTTIOPDACLLOMFATHSLSGMESTVLLAMAFPRYVAICPLRH 135  
QY 72 IISTSPKMLATFWNSTTIOPDACLLOMFATHSLSGMESTVLLAMAFPRYVAICPLRH 135  
DB 136 AATVLTPTKIGVAAVVGALMADLPVFIKQLPFCRSNIISHSYCLHODVKKLACDDT 195  
QY 132 AATVLTPTKIGVAAVVGALMADLPVFIKQLPFCRSNIISHSYCLHODVKKLACDDT 195  
DB 196 RVNVVGLVITISAGLDSLSISFYLLITKTVIGL-TREAQAKAGTCVSHCAVFIFF 254  
QY 192 LPRVNVGLVITISAGLDSLSISFYLLITKTVIGL-TREAQAKAGTCVSHCAVFIFF 254  
DB 255 VPIGLSMVHRSKRSDPLVPLANTYLLVPPVNLPIYGVTKREIRRIELTFVA 312  
QY 252 VPIGLSMVHRSKRSDPLVPLANTYLLVPPVNLPIYGVTKREIRRIELTFVA 312  
DB 252 VPIGLSMVHRSKRSDPLVPLANTYLLVPPVNLPIYGVTKREIRRIELTFVA 312

RESULT 7  
US-08-988-876-7  
; Sequence 7, Application US/08988876  
; Patent No. 6063596  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yee, Henry  
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED  
; TITLE OF INVENTION: WITH IMMUNE RESPONSE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
;; STREET: 3174 Porter Drive  
;; CITY: Palo Alto  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 94304  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: diskette  
;; COMPUTER: IBM compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSeq for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/988,876  
;; FILING DATE: Herewith  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER:  
;; FILING DATE:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Billings, Lucy J.  
;; REGISTRATION NUMBER: 36,749  
;; REFERENCE/DOCKET NUMBER: PF-0441 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650-855-0555  
;; TELEFAX: 650-845-4166  
;; TELEX:  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 314 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; IMMEDIATE SOURCE:  
;; LIBRARY: GenBank  
;; CLONE: 32086  
;; US-08-988-876-7

Query Match 26.6%; Score 431.5; DB 3; Length 314;  
Best Local Similarity 34.8%; Pred. No. 3.8e-32;  
Matches 109; Conservative 63; Mismatches 120; Indels 21; Gaps 8;

DB 8 NESAATFIIIGLGLLEAOWFLAFPLCSLYLNAVGNLTIIYVREHSHHEPMYIFLC 67  
QY 5 NESAATFIIIGLGLLEAOWFLAFPLCSLYLNAVGNLTIIYVREHSHHEPMYIFLC 67  
DB 68 NESAATFIIIGLGLLEAOWFLAFPLCSLYLNAVGNLTIIYVREHSHHEPMYIFLC 67  
QY 65 NESAATFIIIGLGLLEAOWFLAFPLCSLYLNAVGNLTIIYVREHSHHEPMYIFLC 67  
DB 128 AICPRL-HYRAMSPMLCALVALSWLTFHMLHTL-LMARLCCADNVIPHFCDM 181  
QY 125 AICPRL-HYRAMSPMLCALVALSWLTFHMLHTL-LMARLCCADNVIPHFCDM 181  
DB 185 ODVKKLACDDIRN-VYGLVITISAGLDSLSISFYLLITKTVIGL-TREAQAK 238  
QY 182 ODVKKLACDDIRN-VYGLVITISAGLDSLSISFYLLITKTVIGL-TREAQAK 238  
DB 239 AFGCVSHVCAVFEYVPIGLSMVHRSKRSDPL-VPLANTYLLVPPVNLPIYGVK 297  
QY 237 AFGCVSHVCAVFEYVPIGLSMVHRSKRSDPL-VPLANTYLLVPPVNLPIYGVK 297  
DB 298 TKEIRRIELTFH 310  
QY 294 TKEIRRIELTFH 310  
DB 294 TKEIRRIELTFH 310

RESULT 8  
US-08-988-876-5  
; Sequence 5, Application US/08988876  
; Patent No. 6063596  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Bandman, Olga

APPLICANT: Hillman, Jennifer L.  
APPLICANT: Yue, Henry  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED  
WITH IMMUNE RESPONSE  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,876  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0441 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 309 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1314667  
US-08-988-876-5

Query Match 24.6%; Score 398.5; DB 3; Length 309;  
Best Local Similarity 29.3%; Pred. No. 4e-29;  
Matches 88; Conservative 75; Mismatches 126; Indels 11; Gaps 5;

QY 8 NNESSATYFIIIGLPGEAQMFLAPPLCSLYLNAVGNLTIIYIVRTEHSLHEPMYIFLC 67  
DB 5 NDRTRPEFLILGFESEPRLOPFLGFLSMYLVTLISNMLLILNAVSSDSHATPMYIFFLA 64  
QY 68 MLSGIDILISTSMAPKMLAIWFNSTTIQPDACILQMFALHSLSGMESTVLLMAAFDRYV 127  
DB 65 NLSFVDFICFTCTIPKMLVNIQTOKRYTVESCIQMTFFELFAGIDNFLTVAAYDRYM 124  
QY 128 AICHPRLHATVLTLPRTYKIGVAAVVGAAALMAPLPYFIKQLPFCRSNLIISYCLADYV 187  
DB 125 AICGPHLHATVMTNPOCLSLLLVSWINSALHSLLOTLAVLRISFCTHQPDPHFCELMNOM 184  
QY 188 MKLACDDIRVN--VYGLIVITSAIGDSLISFSYLLILKTVLGL--TREDAKAFGTCV 244  
DB 185 IQLACSTFLNNMMLYFAAILLGAFLVGV--YSFKIVSSIKGISAHSKYKAFSTCA 242  
QY 245 SHCAVFIFYPPETG--LSMVHRSKRDSPLPYILANITYLVPEVLPNPIYGVGTEKIR 302  
DB 243 SHLSVSVLSFCTSLGVLVLSAAPTSTHSS----VASVMTYVWVPMNLNPFYISLKNQIK 298

RESULT 9  
US-08-988-876-6  
Sequence 6, Application us/08988876  
Patent No. 6063596  
GENERAL INFORMATION:

APPLICANT: Lal, Preeti  
APPLICANT: Bandman, Olga  
APPLICANT: Hillman, Jennifer L.  
APPLICANT: Yue, Henry  
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED  
WITH IMMUNE RESPONSE  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/988,876  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0441 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 333 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 205814  
US-08-988-876-6

Query Match 23.4%; Score 380; DB 3; Length 333;  
Best Local Similarity 28.0%; Pred. No. 2.2e-27;  
Matches 93; Conservative 74; Mismatches 133; Indels 32; Gaps 9;

QY 6 NNESSATYFIIIGLPGEAQMFLAPPLCSLYLNAVGNLTIIYIVRTEHSLHEPMYIF 65  
DB 3 SNRTRVSEFLILGFEVENDLOPLIYGLFLSMYLVINISITVAIISDPCLHPTMYEF 62  
QY 66 LCMGIDILISTSMAPKMLAIWFNSTTIQPDACILQMFALHSLSGMESTVLLMAAFDR 125  
DB 63 LSNLSFVDFICFTCTIPKMLVNIQTOKRYTVESCIQMTFFELFAGIDNFLTVAAYDR 122  
QY 136 YVAICHPRLHATVLTLP---RYTKIGVAAVVGAAALMAPLPYFIKQLPFCRSNLIISHSY 181  
DB 123 YVAICHPHMYTVINMYKLGFLVIVSWIVSLH--ALPQSL--MMLALPFCHELEPHVF 178  
QY 182 CLHDDVMKLACDDIRVN--VYGLIVITSAIGDSLISFSYLLILKTVLGL--EAQAK 238  
DB 179 CBNQVOIOLTCSDAFLNDVIFYFTVLATVPLAG--IFYSVKIVSSICAISVVGKRYK 236  
QY 239 AFGCVSHCAVFIFYPPETG--LSMVHRSKRDSPLPYILANITYLVPEVLPNPIYGVG 297  
DB 237 AFTCASHLSVSVLSFCTGLG--VYLSAANNSSQASATASVMTVTPVWNPFIYSIK 293  
QY 298 TKRIRO-----NRLRLEHVATH 314  
DB 294 NDKVSVLKTKICEVIRISPLHLHFLVICH 325



DB 241 FSTCSSLVCVGLFSGSAIWMYMAK-SRHEEQKYLELILFLSTPMKAP 291

RESULT 12  
US-08-465-980-3

; Sequence 3, Application US/08465980

; Patent No. 5756309

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel R.

; APPLICANT: LI, YI

; APPLICANT: Rosen, Craig A.

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CROCHT,

; ADDRESSEE: STUART & OLSTEIN

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Ferraro, Gregory D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-446

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 247 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-465-980-3

Query Match 22.3%; Score 361.5; DB 1; Length 247;  
Best Local Similarity 36.9%; Pred. No. 7.7e-26;  
Matches 94; Conservative 45; Mismatches 99; Indels 17; Gaps 6;

QY 15 FILIGDLEBQFMAFPLCSLYLVNLTIIYVREHSLHEPMTIFLCMSGIDI 74  
DB 1 FILIGDLEBQFMAFPLCSLYLVNLTIIYVREHSLHEPMTIFLCMSGIDI 60  
QY 75 LISTSMKMLAIWFNSTIOPDACLLOWFAHSLSGMESTVLLAAMDYVAICHLR 134  
DB 61 CFSSVTIPKLLQNMQNDPSIPADCLTOMFLLFGDLESFLVAAAYDXYVAICPL- 119  
QY 135 HATVLTLPRTYKIGVA--AVRGAALAPLPVFIKOLPFGRNLSHSYCIHODVAKLA 191  
DB 120 HYTAIMPMLCALVALSWVITTFHAMLHTL--LMARLCFQADVVIHFPCDMGALAKLA 177  
QY 192 CDDIRVN----VYGLIIVISAIGDSLISFSYLLILKTVGL--TREDAKAFGCVS 245  
DB 178 FSDTRVNEWVFIIMGILIVY----PFLILIGSYARIVSILKVPSSKGICKAFSTGCS 232  
QY 246 HVCATFEYVPTGL 260  
DB 233 HLSVSLFTGTIGL 247

RESULT 13

US-09-053-303-3  
; Sequence 3, Application US/09053303

; Patent No. 5948890

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel R.

; APPLICANT: LI, YI

; APPLICANT: Rosen, Craig A.

; APPLICANT: Ruben, Steven M.

; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CROCHT,

; ADDRESSEE: STUART & OLSTEIN

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Ferraro, Gregory D.

; REGISTRATION NUMBER: 36,134

; REFERENCE/DOCKET NUMBER: 325800-446

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 247 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-053-303-3

Query Match 22.3%; Score 361.5; DB 2; Length 247;  
Best Local Similarity 36.9%; Pred. No. 7.7e-26;  
Matches 94; Conservative 45; Mismatches 99; Indels 17; Gaps 6;

QY 15 FILIGDLEBQFMAFPLCSLYLVNLTIIYVREHSLHEPMTIFLCMSGIDI 74  
DB 1 FILIGDLEBQFMAFPLCSLYLVNLTIIYVREHSLHEPMTIFLCMSGIDI 60  
QY 75 LISTSMKMLAIWFNSTIOPDACLLOWFAHSLSGMESTVLLAAMDYVAICHLR 134  
DB 61 CFSSVTIPKLLQNMQNDPSIPADCLTOMFLLFGDLESFLVAAAYDXYVAICPL- 119  
QY 135 HATVLTLPRTYKIGVA--AVRGAALAPLPVFIKOLPFGRNLSHSYCIHODVAKLA 191  
DB 120 HYTAIMPMLCALVALSWVITTFHAMLHTL--LMARLCFQADVVIHFPCDMGALAKLA 177  
QY 192 CDDIRVN----VYGLIIVISAIGDSLISFSYLLILKTVGL--TREDAKAFGCVS 245  
DB 178 FSDTRVNEWVFIIMGILIVY----PFLILIGSYARIVSILKVPSSKGICKAFSTGCS 232  
QY 246 HVCATFEYVPTGL 260  
DB 233 HLSVSLFTGTIGL 247

RESULT 14  
US-09-339-115-3

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; Sequence 3, Application US/09339115
; Patent No. 6372891
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Li, Yi
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRJ70
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/339,115
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/053,303
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-339-115-3

Query Match 22.3%; Score 361.5; DB 4; Length 247;
Best Local Similarity 36.9%; Pred. No. 7.7e-26;
Matches 94; Conservative 45; Mismatches 99; Indels 17; Gaps 6;

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DB 1 FILIGLPGLEAQMFLAFLCSLYLAVGNLTIIYVREHSLHEPMYIFLCMLSGIDI 60
QY 75 LISTSSPKMLATFWNSTTIOFDACILQWFAIHSLSGSESTVLLMAFDRYVAICPLR 134
DB 61 CFSSVTIPKILQNMQNDPSIPYADCTQWYFLLFGDLESFLLVMAAYDRYVAICPL- 119
QY 135 HATVLTIPRTKIGVA--AVRGALMAPLPVFIKOLPCRSNIIISHSYCLHDVAKLA 191
DB 120 HYTAIMSPMLCALVALSWLTFTHAMLT--LMAKLCPCADNVIPHFCDMSALAKLA 177
QY 192 CDDIRVN----VYGLIVITSAIGDSLISFSYLLIKTVLGL--TREQAARFGCVS 245
DB 178 FSDIRVNEWYIFIMGLIIVY-----PFLILISYARIVSSILKVPSSKGIKAFSTCGS 232
QY 246 HVCAPFIYVPTGL 260
DB 233 HLSVSLFYGTVIGL 247
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RESULT 15
PCT-US95-07093-3
; Sequence 3, Application PC/TUS9507093
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; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Li, Yi
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRJ70
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07093
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,980
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-07093-3

Query Match 22.3%; Score 361.5; DB 5; Length 247;
Best Local Similarity 36.9%; Pred. No. 7.7e-26;
Matches 94; Conservative 45; Mismatches 99; Indels 17; Gaps 6;

QY 15 FILIGLPGLEAQMFLAFLCSLYLAVGNLTIIYVREHSLHEPMYIFLCMLSGIDI 74
DB 1 FILIGLPGLEAQMFLAFLCSLYLAVGNLTIIYVREHSLHEPMYIFLCMLSGIDI 60
QY 75 LISTSSPKMLATFWNSTTIOFDACILQWFAIHSLSGSESTVLLMAFDRYVAICPLR 134
DB 61 CFSSVTIPKILQNMQNDPSIPYADCTQWYFLLFGDLESFLLVMAAYDRYVAICPL- 119
QY 135 HATVLTIPRTKIGVA--AVRGALMAPLPVFIKOLPCRSNIIISHSYCLHDVAKLA 191
DB 120 HYTAIMSPMLCALVALSWLTFTHAMLT--LMAKLCPCADNVIPHFCDMSALAKLA 177
QY 192 CDDIRVN----VYGLIVITSAIGDSLISFSYLLIKTVLGL--TREQAARFGCVS 245
DB 178 FSDIRVNEWYIFIMGLIIVY-----PFLILISYARIVSSILKVPSSKGIKAFSTCGS 232
QY 246 HVCAPFIYVPTGL 260
DB 233 HLSVSLFYGTVIGL 247
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Search completed: March 26, 2003, 09:58:02
Job time : 29 secs
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GenCore version 5.1.4.p5\_4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 26, 2003, 09:58:08 ; Search time 15 seconds  
(without alignments)  
1244.942 Million cell updates/sec

Title: US-09-966-459A-2  
Perfect score: 1623  
Sequence: 1 MAMPNGNESSATFYFILLGL.....KEIRRIIRLRFVATHASRP 318

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 237916 seqs, 58723674 residues

Total number of hits satisfying chosen parameters: 237916

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA.\*  
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2: /cgn2\_6/ptodata/1/pubpaa/RCI\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
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9: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
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12: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1623	100.0	318 9 US-10-012-896-920	Sequence 920, App
2	1623	100.0	318 9 US-09-895-793-920	Sequence 920, App
3	1623	100.0	318 9 US-09-895-814-920	Sequence 920, App
4	1623	100.0	318 9 US-09-966-459A-2	Sequence 2, Appl
5	1623	100.0	318 10 US-09-753-143-920	Sequence 920, App
6	1623	100.0	318 10 US-09-780-669-920	Sequence 920, App
7	1623	100.0	318 10 US-09-823-827-920	Sequence 920, App
8	1623	100.0	318 10 US-09-886-055-91	Sequence 91, Appl
9	983	60.6	320 9 US-09-968-033C-4	Sequence 4, Appl
10	983	60.6	320 9 US-10-012-896-527	Sequence 527, App
11	983	60.6	320 9 US-09-895-793-527	Sequence 527, App
12	983	60.6	320 9 US-09-895-814-527	Sequence 527, App
13	983	60.6	320 10 US-09-753-143-527	Sequence 527, App
14	983	60.6	320 10 US-09-730-018-7	Sequence 7, Appl
15	983	60.6	320 10 US-09-780-669-527	Sequence 527, App
16	983	60.6	320 10 US-09-823-827-527	Sequence 527, App
17	983	60.6	320 10 US-09-886-055-83	Sequence 83, Appl
18	981	60.4	320 9 US-09-966-459A-12	Sequence 12, Appl
19	969.5	59.7	320 9 US-09-968-033C-2	Sequence 2, Appl

## ALIGNMENTS

20	968.5	59.7	320 12 US-10-079-719-2	Sequence 2, Appl
21	941.5	58.0	324 10 US-09-886-055-81	Sequence 81, Appl
22	892.5	55.0	314 10 US-09-886-055-335	Sequence 335, App
23	872.5	53.8	312 10 US-09-886-055-265	Sequence 265, App
24	845.5	52.1	329 10 US-09-886-055-261	Sequence 261, App
25	828	51.0	317 10 US-09-886-055-93	Sequence 93, Appl
26	827.5	51.0	315 10 US-09-886-055-107	Sequence 107, App
27	820	50.5	319 9 US-09-966-459A-11	Sequence 11, Appl
28	818.5	50.4	314 10 US-09-886-055-85	Sequence 85, Appl
29	818	50.4	313 10 US-09-886-055-115	Sequence 115, App
30	817.5	50.4	314 9 US-10-032-106-10	Sequence 10, Appl
31	817.5	50.4	314 10 US-09-886-055-89	Sequence 89, App
32	815	50.2	321 10 US-09-886-055-117	Sequence 117, App
33	815	50.2	321 10 US-09-886-055-117	Sequence 259, App
34	810.5	49.9	314 10 US-09-886-055-263	Sequence 263, App
35	807	49.7	326 9 US-09-966-459A-14	Sequence 14, Appl
36	803	49.5	312 10 US-09-886-055-487	Sequence 487, App
37	802.5	49.4	312 10 US-09-886-055-333	Sequence 333, App
38	800	49.3	302 10 US-09-886-055-337	Sequence 337, App
39	796.5	49.1	318 10 US-09-886-055-101	Sequence 101, App
40	794.5	49.0	324 10 US-09-886-055-219	Sequence 219, App
41	788	48.6	313 10 US-09-886-055-111	Sequence 111, App
42	784	48.3	344 10 US-09-886-055-341	Sequence 341, App
43	782.5	48.2	307 9 US-09-966-459A-9	Sequence 9, Appl
44	782.5	48.2	326 10 US-09-886-055-267	Sequence 267, App
45	775	47.8	311 10 US-09-886-055-113	Sequence 113, App

RESULT 1  
US-10-012-896-920  
Sequence 920, Application US/10012896  
Publication No. US20020183251A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiansheng  
APPLICANT: Dillon, David C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yugu  
APPLICANT: Kalos, Michael D.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Derrick  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Hurral, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Vinals de Bassols, Carlota  
APPLICANT: Foy, Teresa  
APPLICANT: Fanger, Gary R.  
APPLICANT: Mantanabe, Yoshihiro  
APPLICANT: Meagher, Madeleine Joy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER  
FILE REFERENCE: 210121.427C27  
CURRENT APPLICATION NUMBER: US/10/012.896  
CURRENT FILING DATE: 2001-12-10  
NUMBER OF SEQ ID NOS: 1011  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 920  
LENGTH: 318  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-012-896-920

Query Match 100.0%; Score 1623; DB 9; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-147;  
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMDNGNESSATYFTLLIGLPGLEAOFWLAFLPCLSLYLAVGNLTIIYVTEHSLH 60  
 DB 1 MAMDNGNESSATYFTLLIGLPGLEAOFWLAFLPCLSLYLAVGNLTIIYVTEHSLH 60  
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 DB 61 PMTIFCLMSGIDILISTSSMPKMLAIFWNSTTIOFDACLLQMPAHSLSGNESTVLLA 120  
 QY 121 MAFDRVVAICHPLRHATVLTLPRTKIGVAAVYRGAAALMAPLVPFTKOLPFCRSNLSHS 180  
 DB 121 MAFDRVVAICHPLRHATVLTLPRTKIGVAAVYRGAAALMAPLVPFTKOLPFCRSNLSHS 180  
 QY 181 YCHADQVKMLACDDIRVNVVYGLIYIISAIGDSLISPSYLLILKTVLGLTREAQAKAF 240  
 DB 181 YCHADQVKMLACDDIRVNVVYGLIYIISAIGDSLISPSYLLILKTVLGLTREAQAKAF 240  
 QY 241 GTCVSHVCAVFITYVPFGLSMVHRFSKRDSPLPYILANIYLLVPPVLPNPIYGVKTRK 300  
 DB 241 GTCVSHVCAVFITYVPFGLSMVHRFSKRDSPLPYILANIYLLVPPVLPNPIYGVKTRK 300  
 QY 301 IRORIILRFHVATHASEP 318  
 DB 301 IRORIILRFHVATHASEP 318

# RESULT 2

US-09-895-793-920  
 ; Sequence 920, Application US/09895793  
 ; Publication No. US20020192763A1

## GENERAL INFORMATION:

;; APPLICANT: Xu, Jiangchun  
 ;; APPLICANT: Dillon, Davin C.  
 ;; APPLICANT: Mitcham, Jennifer L.  
 ;; APPLICANT: Harlocker, Susan L.  
 ;; APPLICANT: Jiang, Yugu  
 ;; APPLICANT: Kalos, Michael D.  
 ;; APPLICANT: Retter, Marc W.  
 ;; APPLICANT: Stolk, John A.  
 ;; APPLICANT: Day, Craig H.  
 ;; APPLICANT: Vedvick, Thomas S.  
 ;; APPLICANT: Carter, Darlick  
 ;; APPLICANT: Li, Samuel X.  
 ;; APPLICANT: Wang, Aljun  
 ;; APPLICANT: Skelky, Yasir A.W.  
 ;; APPLICANT: Hepler, William T.  
 ;; APPLICANT: Henderson, Robert A.  
 ;; APPLICANT: Hural, John  
 ;; APPLICANT: McNeill, Patricia D.  
 ;; APPLICANT: Houghton, Raymond L.  
 ;; APPLICANT: Vinals de Bassols, Carlota  
 ;; APPLICANT: Foy, Teresa  
 ;; APPLICANT: Fanger, Gary R.  
 ;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ;; FILE REFERENCE: 210121.534C2  
 ;; CURRENT APPLICATION NUMBER: US/09/895,793  
 ;; CURRENT FILING DATE: 2001-06-29  
 ;; NUMBER OF SEQ ID NOS: 982  
 ;; SOFTWARE: FastSeq for Windows Version 3.0  
 ;; SEQ ID NO 920  
 ;; LENGTH: 318  
 ;; TYPE: PRT  
 ;; ORGANISM: Homo sapiens  
 US-09-895-793-920

Query Match 100.0%; Score 1623; DB 9; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-147;  
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMDNGNESSATYFTLLIGLPGLEAOFWLAFLPCLSLYLAVGNLTIIYVTEHSLH 60  
 DB 1 MAMDNGNESSATYFTLLIGLPGLEAOFWLAFLPCLSLYLAVGNLTIIYVTEHSLH 60  
 QY 61 PMTIFCLMSGIDILISTSSMPKMLAIFWNSTTIOFDACLLQMPAHSLSGNESTVLLA 120  
 DB 61 PMTIFCLMSGIDILISTSSMPKMLAIFWNSTTIOFDACLLQMPAHSLSGNESTVLLA 120  
 QY 121 MAFDRVVAICHPLRHATVLTLPRTKIGVAAVYRGAAALMAPLVPFTKOLPFCRSNLSHS 180  
 DB 121 MAFDRVVAICHPLRHATVLTLPRTKIGVAAVYRGAAALMAPLVPFTKOLPFCRSNLSHS 180  
 QY 181 YCHADQVKMLACDDIRVNVVYGLIYIISAIGDSLISPSYLLILKTVLGLTREAQAKAF 240  
 DB 181 YCHADQVKMLACDDIRVNVVYGLIYIISAIGDSLISPSYLLILKTVLGLTREAQAKAF 240  
 QY 241 GTCVSHVCAVFITYVPFGLSMVHRFSKRDSPLPYILANIYLLVPPVLPNPIYGVKTRK 300  
 DB 241 GTCVSHVCAVFITYVPFGLSMVHRFSKRDSPLPYILANIYLLVPPVLPNPIYGVKTRK 300  
 QY 301 IRORIILRFHVATHASEP 318  
 DB 301 IRORIILRFHVATHASEP 318

# RESULT 3

US-09-895-814-920  
 ; Sequence 920, Application US/09895814  
 ; Publication No. US20020193296A1

## GENERAL INFORMATION:

;; APPLICANT: Xu, Jiangchun  
 ;; APPLICANT: Dillon, Davin C.  
 ;; APPLICANT: Mitcham, Jennifer L.  
 ;; APPLICANT: Harlocker, Susan L.  
 ;; APPLICANT: Jiang, Yugu  
 ;; APPLICANT: Kalos, Michael D.  
 ;; APPLICANT: Retter, Marc W.  
 ;; APPLICANT: Stolk, John A.  
 ;; APPLICANT: Day, Craig H.  
 ;; APPLICANT: Vedvick, Thomas S.  
 ;; APPLICANT: Carter, Darlick  
 ;; APPLICANT: Li, Samuel X.  
 ;; APPLICANT: Wang, Aljun  
 ;; APPLICANT: Skelky, Yasir A.W.  
 ;; APPLICANT: Hepler, William T.  
 ;; APPLICANT: Henderson, Robert A.  
 ;; APPLICANT: Hural, John  
 ;; APPLICANT: McNeill, Patricia D.  
 ;; APPLICANT: Houghton, Raymond L.  
 ;; APPLICANT: Vinals de Bassols, Carlota  
 ;; APPLICANT: Foy, Teresa  
 ;; APPLICANT: Fanger, Gary R.  
 ;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
 ;; FILE REFERENCE: 210121.427C26  
 ;; CURRENT APPLICATION NUMBER: US/09/895,814  
 ;; CURRENT FILING DATE: 2001-06-29  
 ;; NUMBER OF SEQ ID NOS: 990  
 ;; SOFTWARE: FastSeq for Windows Version 3.0  
 ;; SEQ ID NO 920  
 ;; LENGTH: 318  
 ;; TYPE: PRT  
 ;; ORGANISM: Homo sapiens  
 US-09-895-814-920

Query Match 100.0%; Score 1623; DB 9; Length 318;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-147;  
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMDNGNESSATYFTLLIGLPGLEAOFWLAFLPCLSLYLAVGNLTIIYVTEHSLH 60  
 DB 1 MAMDNGNESSATYFTLLIGLPGLEAOFWLAFLPCLSLYLAVGNLTIIYVTEHSLH 60

QY 61 PMTIFLCMISGIDILISTSSMPKMLAFMFNSTTIOFDACILQMFALHSISGMESTVLLA 120  
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DB 181 YCLHODVWKACDDIRVNVVYGLIYIISAIGDLSLISFSTLLIKTVLGLTREAOAKAF 240  
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DB 241 GTCVSHCAVEIFVYFPGLSMVRHFRSKRSDPLVLIANTYLLVPPVLPNVGVKTKRE 300  
QY 301 IRORIILRFHVATHASEP 318  
DB 301 IRORIILRFHVATHASEP 318

## RESULT 4

US-09-966-459a-2  
; Sequence 2, Application US/09966459A  
; Publication No. US20030022237A1  
; GENERAL INFORMATION:  
; APPLICANT: FEDER, J.N.  
; APPLICANT: MINTIER, G.  
; APPLICANT: RAMANTHAN, C.S.  
; APPLICANT: HAKEN, D.R.  
; APPLICANT: CACACE, A.  
; APPLICANT: BARBER, L.  
; APPLICANT: KORNACKER, M.G.  
; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HSPRBYT4,  
; FILE REFERENCE: D0039NP  
; CURRENT APPLICATION NUMBER: US/09/966,459A  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 60/235,833  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/261,776  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 60/305,351  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: 60/313,202  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patent Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-966-459a-2

Query Match 100.0%; Score 1623; DB 9; Length 318;  
Best Local Similarity 100.0%; Pred. No. 2.5e-147;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MAFDRYAICHPLRHATVLTLPRTYKIGVAAVVGAAALMAPLPFIRKOLPCRSNIIISHS 180  
QY 181 YCLHODVWKACDDIRVNVVYGLIYIISAIGDLSLISFSTLLIKTVLGLTREAOAKAF 240  
DB 181 YCLHODVWKACDDIRVNVVYGLIYIISAIGDLSLISFSTLLIKTVLGLTREAOAKAF 240

QY 241 GTCVSHCAVEIFVYFPGLSMVRHFRSKRSDPLVLIANTYLLVPPVLPNVGVKTKRE 300  
DB 241 GTCVSHCAVEIFVYFPGLSMVRHFRSKRSDPLVLIANTYLLVPPVLPNVGVKTKRE 300  
QY 301 IRORIILRFHVATHASEP 318  
DB 301 IRORIILRFHVATHASEP 318

## RESULT 5

US-09-759-143-920  
; Sequence 920, Application US/09759143  
; Patent No. US20020022248A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Jiangchun  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Mitcham, Jennifer L.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Jiang, Yugu  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Stolk, John A.  
; APPLICANT: Day, Craig H.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darick  
; APPLICANT: Li, Samuel  
; APPLICANT: Wang, Aljun A.W.  
; APPLICANT: Hepler, William  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.427C23  
; CURRENT APPLICATION NUMBER: US/09/759,143  
; NUMBER OF SEQ ID NOS: 934  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 920  
; LENGTH: 318  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-759-143-920

Query Match 100.0%; Score 1623; DB 10; Length 318;  
Best Local Similarity 100.0%; Pred. No. 2.5e-147;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAFDRYAICHPLRHATVLTLPRTYKIGVAAVVGAAALMAPLPFIRKOLPCRSNIIISHS 180  
DB 1 MAFDRYAICHPLRHATVLTLPRTYKIGVAAVVGAAALMAPLPFIRKOLPCRSNIIISHS 180  
QY 181 YCLHODVWKACDDIRVNVVYGLIYIISAIGDLSLISFSTLLIKTVLGLTREAOAKAF 240  
DB 181 YCLHODVWKACDDIRVNVVYGLIYIISAIGDLSLISFSTLLIKTVLGLTREAOAKAF 240  
QY 241 GTCVSHCAVEIFVYFPGLSMVRHFRSKRSDPLVLIANTYLLVPPVLPNVGVKTKRE 300  
DB 241 GTCVSHCAVEIFVYFPGLSMVRHFRSKRSDPLVLIANTYLLVPPVLPNVGVKTKRE 300  
QY 301 IRORIILRFHVATHASEP 318  
DB 301 IRORIILRFHVATHASEP 318

## RESULT 6

US-09-780-669-920

; Sequence 920, Application US/09780669

; Patent No. US20020051977A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqun

; APPLICANT: Henderson, Robert A.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Panger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darriack

; APPLICANT: Li, Samuel

; APPLICANT: Wang, Ajun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; APPLICANT: Hurai, John

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Houghton, Raymond L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.427C24

; CURRENT APPLICATION NUMBER: US/09/780,669

; CURRENT FILING DATE: 2001-02-09

; NUMBER OF SEQ ID NOS: 943

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 920

; LENGTH: 318

; TYPE: PRF

; ORGANISM: Homo sapiens

; US-09-780-669-920

Query Match 100.0%; Score 1623; DB 10; Length 318;  
Best Local Similarity 100.0%; Pred. No. 2.5e-147;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYDPNGNESSATYFLLIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSLH 60  
DB 1 MMYDPNGNESSATYFLLIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSLH 60  
QY 61 PNYIFLCMLSGIDILISTSSMPKMLAFWENSTTIOFDACLLQMFALHSLSGNESTVLA 120  
DB 61 PNYIFLCMLSGIDILISTSSMPKMLAFWENSTTIOFDACLLQMFALHSLSGNESTVLA 120  
QY 121 MMDRYVAICHPRHATVTLPRVTIKGVAAYVGAALAMPVFTKOLPFCRSNIISHS 180  
DB 121 MMDRYVAICHPRHATVTLPRVTIKGVAAYVGAALAMPVFTKOLPFCRSNIISHS 180  
QY 181 YCHLQDVYKACDIDIRNVYVGLIIVISAIGDSLISFYLILKTVLGLTREAQKAF 240  
DB 181 YCHLQDVYKACDIDIRNVYVGLIIVISAIGDSLISFYLILKTVLGLTREAQKAF 240  
QY 241 GTCVSHVCAVFIFYVPFGLSMVHRSKRSDPLVITANIYLLVPPVLPYGVATKE 300  
DB 241 GTCVSHVCAVFIFYVPFGLSMVHRSKRSDPLVITANIYLLVPPVLPYGVATKE 300  
QY 301 IRORIILRFHVAHASEP 318  
DB 301 IRORIILRFHVAHASEP 318

## RESULT 7

US-09-822-827-920

; Sequence 920, Application US/09822827

; Patent No. US20020081680A1

; GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.534C1  
CURRENT APPLICATION NUMBER: US/09/822,827  
CURRENT FILING DATE: 2001-03-28  
NUMBER OF SEQ ID NOS: 982  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 920  
LENGTH: 318  
TYPE: PRF  
ORGANISM: Homo sapiens  
US-09-822-827-920

Query Match 100.0%; Score 1623; DB 10; Length 318;  
Best Local Similarity 100.0%; Pred. No. 2.5e-147;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYDPNGNESSATYFLLIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSLH 60  
DB 1 MMYDPNGNESSATYFLLIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSLH 60  
QY 61 PNYIFLCMLSGIDILISTSSMPKMLAFWENSTTIOFDACLLQMFALHSLSGNESTVLA 120  
DB 61 PNYIFLCMLSGIDILISTSSMPKMLAFWENSTTIOFDACLLQMFALHSLSGNESTVLA 120  
QY 121 MMDRYVAICHPRHATVTLPRVTIKGVAAYVGAALAMPVFTKOLPFCRSNIISHS 180  
DB 121 MMDRYVAICHPRHATVTLPRVTIKGVAAYVGAALAMPVFTKOLPFCRSNIISHS 180  
QY 181 YCHLQDVYKACDIDIRNVYVGLIIVISAIGDSLISFYLILKTVLGLTREAQKAF 240  
DB 181 YCHLQDVYKACDIDIRNVYVGLIIVISAIGDSLISFYLILKTVLGLTREAQKAF 240  
QY 241 GTCVSHVCAVFIFYVPFGLSMVHRSKRSDPLVITANIYLLVPPVLPYGVATKE 300  
DB 241 GTCVSHVCAVFIFYVPFGLSMVHRSKRSDPLVITANIYLLVPPVLPYGVATKE 300  
QY 301 IRORIILRFHVAHASEP 318  
DB 301 IRORIILRFHVAHASEP 318

## RESULT 8

US-09-886-055-91

; Sequence 91, Application US/09886055

; Patent No. US20020132273A1

; GENERAL INFORMATION:

; APPLICANT: STRYER, LUBERT

; APPLICANT: KOZUYA, SERGEY

; TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND

; FILE REFERENCE: 078003-0277150

; CURRENT APPLICATION NUMBER: US/09/886,055

; CURRENT FILING DATE: 2001-06-22

; PRIOR APPLICATION NUMBER: 60/213,812

; NUMBER OF SEQ ID NOS: 522

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 91

; LENGTH: 318

; TYPE: PRF

; ORGANISM: Homo sapiens

; US-09-886-055-91

Query Match 100.0%; Score 1623; DB 10; Length 318;  
Best Local Similarity 100.0%; Pred. No. 2.5e-147;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMYDPNGNESSATYFLLIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSLH 60  
DB 1 MMYDPNGNESSATYFLLIGLPGLEAOFMLAFPLCSLYLAVGNLTIIYVTEHSLH 60

QY 61 PATIFLCMISGIDILISTSSMPKMLAFWENSTTIOFDACILQMFALHSISGMSFVTLA 120  
DB 61 PATIFLCMISGIDILISTSSMPKMLAFWENSTTIOFDACILQMFALHSISGMSFVTLA 120  
QY 121 MAFDRVALCHPRHNAVTLPRVTKIGVAAVVGAAALMAPLVEFKQDFPCRSNLSHS 180  
DB 121 MAFDRVALCHPRHNAVTLPRVTKIGVAAVVGAAALMAPLVEFKQDFPCRSNLSHS 180  
QY 181 YCHADVMKACDIDIRNVVYGLVITISAGDLSLISFYLILKTVGLTREAQAKAF 240  
DB 181 YCHADVMKACDIDIRNVVYGLVITISAGDLSLISFYLILKTVGLTREAQAKAF 240  
QY 241 GFCVSHVCAVFIYVPGISWHRFSKRSDPLVYLANITVLLVPPVLPNIYGVKTK 300  
DB 241 GFCVSHVCAVFIYVPGISWHRFSKRSDPLVYLANITVLLVPPVLPNIYGVKTK 300  
QY 301 IRORIIRLEFVATHASEP 318  
DB 301 IRORIIRLEFVATHASEP 318

RESULT 9  
US-09-966-033C-4  
Sequence 4, Application US/09968033C  
Patent No. US2002016871A1  
GENERAL INFORMATION:  
APPLICANT: Soppet et al.  
TITLE OF INVENTION: Human Prostate Specific G-Protein Receptor HPRMJ70  
FILE REFERENCE: PFI80P1  
CURRENT APPLICATION NUMBER: US/09/968,033C  
PRIOR FILING DATE: 2001-10-02  
PRIOR APPLICATION NUMBER: 60/237,275  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 09/339,115  
PRIOR FILING DATE: 1999-06-24  
PRIOR APPLICATION NUMBER: 09/053,303  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 08/465,980  
PRIOR FILING DATE: 1995-06-06  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Patentln Ver. 2.1  
SEQ ID NO 4  
LENGTH: 320  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-966-033C-4

Query Match 60.6%; Score 983; DB 9; Length 320;  
Best Local Similarity 59.8%; Pred. No. 3, 2e-86;  
Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

QY 8 NBSATYFLLIGLPGLEAQFNLAPPLCSLYLAVGNLTITTYVREHSLHEPMTFLC 67  
DB 5 NBTNAT-FVLLIGLPGLEKAFNFWGFPILSMYVAMGNCIVFIVTERSLHAPMTFLC 63  
QY 68 MLSGIDILISTSSMPKMLAFWENSTTIOFDACILQMFALHSISGMSFVTLA 127  
DB 64 MLAIDLALSTSMKPIALFWDSEISREKLTQMFTHALSAESTILLMAADRYV 123  
QY 128 AICHPLEHNAVTLPRVTKIGVAAVVGAAALMAPLVEFKQDFPCRSNLSHSYCHODV 187  
DB 124 AICHPLEHNAVTLPRVTKIGVAAVVGAAALMAPLVEFKQDFPCRSNLSHSYCHODV 183  
QY 188 MKLACDIDIRNVVYGLVITISAGDLSLISFYLILKTVGLTREAQAKAFGTCVSH 246  
DB 184 MKLAVADTLPRNVVYGLVITISAGDLSLISFYLILKTVGLTREAQAKAFGTCVSH 243  
QY 247 VCAVFEYVPGISWHRFSKRSDPLVYLANITVLLVPPVLPNIYGVKTK 306  
DB 244 IGVYLAFTVPLIGLSVYHRRGNSLHPIYRVVMGDITLLPVPINPIYGAKTQIRTVL 303  
QY 307 RLEFVA 312  
: : :

DB 304 AMFKIS 309

RESULT 10  
US-10-012-896-527  
Sequence 527, Application US/10012896  
Publication No. US20020183251A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jiangchun  
APPLICANT: Dillon, Davin C.  
APPLICANT: Mitchell, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yugu  
APPLICANT: Kalos, Michael D.  
APPLICANT: Reiter, Marc W.  
APPLICANT: Stolk, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aljun  
APPLICANT: Skelky, Yasir A.W.  
APPLICANT: Hepler, William T.  
APPLICANT: Henderson, Robert A.  
APPLICANT: Hurrell, John  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Houghton, Raymond L.  
APPLICANT: Vinals de Bassols, Carlota  
APPLICANT: Foy, Teresa  
APPLICANT: Fanger, Gary R.  
APPLICANT: Mantabe, Yoshihiro  
APPLICANT: Meagher, Madeleine Joy  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427027  
CURRENT APPLICATION NUMBER: US/10/012,896  
CURRENT FILING DATE: 2001-12-10  
NUMBER OF SEQ ID NOS: 1011  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 527  
LENGTH: 320  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-012-896-527

Query Match 60.6%; Score 983; DB 9; Length 320;  
Best Local Similarity 59.8%; Pred. No. 3, 2e-86;  
Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

QY 8 NBSATYFLLIGLPGLEAQFNLAPPLCSLYLAVGNLTITTYVREHSLHEPMTFLC 67  
DB 5 NBTNAT-FVLLIGLPGLEKAFNFWGFPILSMYVAMGNCIVFIVTERSLHAPMTFLC 63  
QY 68 MLSGIDILISTSSMPKMLAFWENSTTIOFDACILQMFALHSISGMSFVTLA 127  
DB 64 MLAIDLALSTSMKPIALFWDSEISREKLTQMFTHALSAESTILLMAADRYV 123  
QY 128 AICHPLEHNAVTLPRVTKIGVAAVVGAAALMAPLVEFKQDFPCRSNLSHSYCHODV 187  
DB 124 AICHPLEHNAVTLPRVTKIGVAAVVGAAALMAPLVEFKQDFPCRSNLSHSYCHODV 183  
QY 188 MKLACDIDIRNVVYGLVITISAGDLSLISFYLILKTVGLTREAQAKAFGTCVSH 246  
DB 184 MKLAVADTLPRNVVYGLVITISAGDLSLISFYLILKTVGLTREAQAKAFGTCVSH 243  
QY 247 VCAVFEYVPGISWHRFSKRSDPLVYLANITVLLVPPVLPNIYGVKTK 306  
DB 244 IGVYLAFTVPLIGLSVYHRRGNSLHPIYRVVMGDITLLPVPINPIYGAKTQIRTVL 303  
QY 307 RLEFVA 312  
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DB 304 AMFKIS 309

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RESULT 11
US-09-895-793-527
; Sequence 527, Application US/09895793
; Publication No. US20020192763a1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 527
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-793-527

Query Match          60.6%; Score 983; DB 9; Length 320;
Best Local Similarity 59.8%; Pred. No. 3.2e-86;
Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

QY 8 NEEAATYFLLIGLPGLEAOFWLAFLPCLSLYLAIVAGNLTIIYVTEHSLHEPMTFLC 67
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 5 NFPHAT-FYLLIGLPGLEKAHFVWGPFLLSYVVAHMGNCIVFIVTERSLHAPMTFLC 63
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 68 MLESGDILISTSMKPMALAFWNSSTTIOFDACLQMFALHSLSGSESYVLLAMADRY 127
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 64 MLAIDLAISTSTMPKTLALFWPDSREISFEACLTQMFHALSAIESYLLAMADRY 123
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 128 AICHPRLHATVLLPRTYKIGVAAVYRGAAALMAPLVEFKOLPFCRSNLTSHSYCLHODV 187
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 124 AICHPRLHAAVLLNNYTAOIGYAAVYRGSLFFPPLILKRLAFCHSNVLSHYCVHODV 183
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 188 MKLACDDIRVNVYGLIIVISAIGDSLISFYLILKTVGL-TREAQAKAFGTCVSH 246
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 184 MKLAAVADTLNPNVYGLTALIVMGVDVMPISLSYFLIRIVQLPSEKSEAKAFGTCVSH 243
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 247 VCAVFIFYVPEIGLSVWHRGSKRSDPLVYLLANTYLLVPVLPVYGVKTEIRQL 306
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 244 IGVYLAIFYVPLIGLSVWHRGSLHPIVRVVMGDYLLPVPINPIYGAKTQIRTVL 303
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 307 RLPHVA 312
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 304 AMFKIS 309
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 12
US-09-895-814-527
; Sequence 527, Application US/09895814
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Publication No. US20020193296A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C26
; CURRENT APPLICATION NUMBER: US/09/895,814
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 990
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 527
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-895-814-527

Query Match          60.6%; Score 983; DB 9; Length 320;
Best Local Similarity 59.8%; Pred. No. 3.2e-86;
Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

QY 8 NEEAATYFLLIGLPGLEAOFWLAFLPCLSLYLAIVAGNLTIIYVTEHSLHEPMTFLC 67
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 5 NFPHAT-FYLLIGLPGLEKAHFVWGPFLLSYVVAHMGNCIVFIVTERSLHAPMTFLC 63
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 68 MLESGDILISTSMKPMALAFWNSSTTIOFDACLQMFALHSLSGSESYVLLAMADRY 127
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 64 MLAIDLAISTSTMPKTLALFWPDSREISFEACLTQMFHALSAIESYLLAMADRY 123
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 128 AICHPRLHATVLLPRTYKIGVAAVYRGAAALMAPLVEFKOLPFCRSNLTSHSYCLHODV 187
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 124 AICHPRLHAAVLLNNYTAOIGYAAVYRGSLFFPPLILKRLAFCHSNVLSHYCVHODV 183
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 188 MKLACDDIRVNVYGLIIVISAIGDSLISFYLILKTVGL-TREAQAKAFGTCVSH 246
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 184 MKLAAVADTLNPNVYGLTALIVMGVDVMPISLSYFLIRIVQLPSEKSEAKAFGTCVSH 243
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 247 VCAVFIFYVPEIGLSVWHRGSKRSDPLVYLLANTYLLVPVLPVYGVKTEIRQL 306
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 244 IGVYLAIFYVPLIGLSVWHRGSLHPIVRVVMGDYLLPVPINPIYGAKTQIRTVL 303
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
QY 307 RLPHVA 312
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB 304 AMFKIS 309
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

RESULT 13
US-09-759-143-527
; Sequence 527, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
```

APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stoik, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: 210121.427C23  
CURRENT APPLICATION NUMBER: US/09/759,143  
CURRENT FILING DATE: 2001-01-12  
NUMBER OF SEQ ID NOS: 934  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 527  
LENGTH: 320  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-759-143-527

Query Match 60.6%; Score 983; DB 10; Length 320;  
Best Local Similarity 59.8%; Pred. No. 3.2e-86;  
Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

QY 8 NESAATYFLLIGLPGLEAOWFMAFPLCSLYIANVGNLTIYRTSHSHEPRTYLC 67  
DB 5 NETAAT-FVLIGPGLERAFHWGFPPLSMYVAMFGNCIYFVYTRERSLAPAPYFLC 63  
QY 68 MLSGIDILISTSMKMLAIFWENSTTIOFACLOMFALHSIGSESTVLLAMAFDRYV 127  
DB 64 MIAADLALSTMKIATLFWDSREISFECLOMFIALHSIESTIILAMAFDRYV 123  
QY 128 AICPELRNAVTLTPRTKIGVAAYVGAALMAPLPEIKOLPECRSNILSHSYCLHODV 187  
DB 124 AICPELRNAVTLNTVTAQIGIVAVRGSLFEFFPLIKRLAFCHSNVLSHSCYHODV 183  
QY 188 MKIACDDIRVNVVGLIYIISAGDSILISPSYLLIKTYGL-TREAOAKAFGTCVSH 246  
DB 184 MKIADADLPVNVVGLIYIISAGDSILISPSYLLIKTYGL-TREAOAKAFGTCVSH 243  
QY 247 VCAREFYVPEFGLSMVRFESKRSDPLVILANITLLVPLNPIYGVTKREIRORIL 306  
DB 244 IGVLAIFYVPLIGLSVHRFGNSLPIRYVWGDYLLPLPINIITIGAKTKOIRTVL 303  
QY 307 RLEHVA 312  
DB 304 AMFKIS 309

RESULT 14  
US-09-730-018-7  
Sequence 7, Application US/09730018  
Patent NO. US2002004877A1  
GENERAL INFORMATION:  
APPLICANT: Ali, Shujath  
APPLICANT: Calferkey, Robert  
APPLICANT: Recipon, Heve  
APPLICANT: Sun, Yongming  
TITLE OF INVENTION: Method of Diagnosing, Monitoring, Staging, Imaging and  
FILE REFERENCE: Treating Prostate Cancer  
CURRENT APPLICATION NUMBER: US/09/730, 018  
CURRENT FILING DATE: 2000-12-04  
PRIOR APPLICATION NUMBER: 60/169,083  
PRIOR FILING DATE: 1999-12-06

NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 320  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-730-018-7

Query Match 60.6%; Score 983; DB 10; Length 320;  
Best Local Similarity 59.8%; Pred. No. 3.2e-86;  
Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

QY 8 NESAATYFLLIGLPGLEAOWFMAFPLCSLYIANVGNLTIYRTSHSHEPRTYLC 67  
DB 5 NETAAT-FVLIGPGLERAFHWGFPPLSMYVAMFGNCIYFVYTRERSLAPAPYFLC 63  
QY 68 MLSGIDILISTSMKMLAIFWENSTTIOFACLOMFALHSIGSESTVLLAMAFDRYV 127  
DB 64 MIAADLALSTMKIATLFWDSREISFECLOMFIALHSIESTIILAMAFDRYV 123  
QY 128 AICPELRNAVTLTPRTKIGVAAYVGAALMAPLPEIKOLPECRSNILSHSYCLHODV 187  
DB 124 AICPELRNAVTLNTVTAQIGIVAVRGSLFEFFPLIKRLAFCHSNVLSHSCYHODV 183  
QY 188 MKIACDDIRVNVVGLIYIISAGDSILISPSYLLIKTYGL-TREAOAKAFGTCVSH 246  
DB 184 MKIADADLPVNVVGLIYIISAGDSILISPSYLLIKTYGL-TREAOAKAFGTCVSH 243  
QY 247 VCAREFYVPEFGLSMVRFESKRSDPLVILANITLLVPLNPIYGVTKREIRORIL 306  
DB 244 IGVLAIFYVPLIGLSVHRFGNSLPIRYVWGDYLLPLPINIITIGAKTKOIRTVL 303  
QY 307 RLEHVA 312  
DB 304 AMFKIS 309

RESULT 15  
US-09-780-669-527  
Sequence 527, Application US/09780669  
Patent NO. US20020051977A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Jlangchun  
APPLICANT: Dillio, David C.  
APPLICANT: Mitcham, Jennifer L.  
APPLICANT: Harlocker, Susan L.  
APPLICANT: Jiang, Yuqi  
APPLICANT: Henderson, Robert A.  
APPLICANT: Kalos, Michael D.  
APPLICANT: Fanger, Gary R.  
APPLICANT: Retter, Marc W.  
APPLICANT: Stoik, John A.  
APPLICANT: Day, Craig H.  
APPLICANT: Vedvick, Thomas S.  
APPLICANT: Carter, Darrick  
APPLICANT: Li, Samuel  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Hepler, William  
APPLICANT: Hural, John  
APPLICANT: McNeill, Patricia D.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
FILE REFERENCE: DIAGNOSIS OF PROSTATE CANCER  
CURRENT APPLICATION NUMBER: US/09/780, 669  
CURRENT FILING DATE: 2001-02-09  
NUMBER OF SEQ ID NOS: 943  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 527  
LENGTH: 320  
TYPE: PRT  
ORGANISM: Homo sapiens

US-09-780-669-527

Query Match 60.6%; Score 983; DB 10; Length 320;  
Best Local Similarity 59.8%; Pred. No. 3.2e-86;  
Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

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QY 8 NESSATYFLLIGLPGLEAQTALAPLPCSLYLAVGNLTIIYIVREHSLHEPMYFLC 67
   | : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 5 NETHAT FVLIGLPGLEKAFMWGFPLLSMYVAMFGNCIYVFIKERSLHAPMILELC 63
   || : || : || : || : || : || : || : || : || : || : || : || : ||
QY 68 MLSGIDILLISTSSMPKMLAFENSTTIOPDACLQMFALHSLSGMESTVLAMAFDRY 127
   || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 64 MLALDIALSTSMPTKILAFWDSREISFEACLTQMFIFHALSAIESTILLAMAFDRY 123
   || : || : || : || : || : || : || : || : || : || : || : || : ||
QY 128 AICHPLRHATVTLPRYTKIGAAVYRGAAALMAPLVYFIKQLPCKSNIIISHYCLHODY 187
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 124 AICHPLRHAAVLANNTVYAOIGIYAVVSGSLFFPPLPLIKRLAFCHSNVLSHSCYHODY 183
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 188 MKLACODIRVNVYVGLIVISATIGDLSLSFSYLILKTVLGL-TREAQAKAFGTCVSH 246
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 184 MKLAVADTLPRNVYGLPAIILVMGVDMFISLSFELIRIVLQLPKSKERAKAFGTCVSH 243
   ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 247 VCAVFIEYVPEFGLSMVHRFSKRSDSPLPYILANITYLLVPPVLPVYVGVTKERIRORIL 306
   : | ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 244 IGVYLAFTYVPLIGLSVYHRRGNSLHPIVRVYMGDIYLLRPVINPIYGAKTQIRTRVL 303
   : | ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
QY 307 RLEHVA 312
   : | : :
Db 304 AMFKIS 309
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Search completed: March 26, 2003, 10:05:08  
Job time : 16 secs



GenCore version 5.1.4 p5.4578  
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OM protein - protein search, using sw model

Run on: March 26, 2003, 09:53:07 ; Search time: 46 Seconds

(without alignments)  
664.581 Million cell updates/sec

Title: US-09-966-459a-2

Perfect score: 1623

Sequence: 1 KMVDPNGNSSATYFILGL.....KEIRKRLRLFNHATHASRP 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

PIR\_73:\*  
1: pirl:\*  
2: pirl2:\*  
3: pirl3:\*  
4: pirl4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	33.9	292	2 A60547	hypothetical prote
2	477.5	29.4	313	2 E45774	odorant receptor 8
3	453	27.9	307	2 S29710	olfactory receptor
4	440	27.1	312	2 A46247	olfactory receptor
5	434.5	26.8	319	2 I23701	olfactory receptor
6	434.5	26.8	312	2 JC5624	olfactory receptor
7	433.5	26.7	312	2 S29708	olfactory receptor
8	432	26.6	328	2 G45774	odorant receptor 2
9	431.5	26.6	310	2 E23701	olfactory receptor
10	431.5	26.6	314	2 S20572	olfactory receptor
11	425.5	26.2	314	2 A37286	olfactory receptor
12	424.5	26.2	321	2 H45774	odorant receptor 3
13	422.5	26.0	305	2 S29711	olfactory factor 0
14	420.5	25.9	314	2 S29707	olfactory receptor
15	418.5	25.8	309	1 S51356	olfactory receptor
16	415	25.6	344	2 I45774	odorant receptor 1
17	413	25.4	312	2 A48413	probable olfactory
18	411.5	25.4	311	2 JC5200	chemoreceptor TB33
19	411	25.3	160	2 S58066	probable olfactory
20	411	25.3	313	2 S20571	olfactory receptor
21	406.5	25.0	311	2 C23701	olfactory receptor
22	405	25.0	317	2 E45774	odorant receptor 4
23	404.5	24.9	313	2 B23701	olfactory receptor
24	401.5	24.7	312	2 G23701	olfactory receptor
25	399.5	24.6	314	2 H23701	olfactory receptor
26	399.5	24.6	328	2 A45774	odorant receptor 3
27	399.5	24.6	328	2 D45774	odorant receptor 3
28	397.5	24.5	328	2 H45774	odorant receptor 3
29	394.5	24.3	320	2 S20573	olfactory receptor

30	393.5	24.2	316	2 A57069	olfactory receptor
31	388.5	23.9	315	2 JC5836	olfactory receptor
32	387.5	23.9	328	2 C45774	odorant receptor 3
33	386.5	23.8	304	2 S29709	olfactory receptor
34	386.5	23.8	312	2 A46750	olfactory receptor
35	380	23.4	333	2 A23701	olfactory receptor
36	379.5	23.4	337	2 E23701	olfactory receptor
37	379	23.4	317	2 D23701	olfactory receptor
38	371.5	22.9	315	2 JC4658	olfactory receptor
39	370	22.8	315	2 JC5201	chemoreceptor TB56
40	366	22.6	318	2 JC5202	chemoreceptor TB64
41	310.5	19.1	222	2 B40745	odorant receptor (
42	310.5	19.1	234	2 S29000	g protein-coupled
43	307.5	18.9	264	2 PC4369	olfactory receptor
44	289.5	17.8	234	2 S28999	g protein-coupled
45	285.5	17.6	222	2 D40745	odorant receptor (

#### ALIGNMENTS

##### RESULT 1

A60547 hypothetical protein (HPFH breakpoint 3' region) - human (fragment)

N:Alternate names: Olfactory receptor homolog

C:Species: Homo sapiens (man)

C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 26-Aug-1999

C:Accession: A60547; A60482

R:Reingold, E.A.; Forget, B.G.

Blood 74, 2178-2186, 1989

A:Title: The breakpoint of a large deletion causing hereditary persistence of fetal

A:Reference number: A60547, MIMD:90028751, PMID:2478223

A:Accession: A60547

A:Molecule type: DNA

A:Residues: 1-292 <FEI>

C:Superfamily: Olfactory receptor OR14

Query Match 33.9%; Score 551; DB 2; Length 292;  
Best local Similarity 41.0%; Pred. No. 1.8e-41;  
Matches 114; Conservative 50; Mismatches 92; Indels 22; Gaps 6;

QY	17	LIGLPGLEAOFMLAPFLCSLYLAVLGNLTIVYTESLSLEPNTIFCLMSGIDILI	76
DB	29	LVGIPGLESLVQCNIQIGFCAIYLILAMIGNSLISIKERSLSHEPLTIFLNGATGATIAL	88
QY	77	STSGMPMLAIFPENS-TTIOFDACLOMFAIR-SLSGMSYVLLAMAFRYVAICPLR	134
DB	89	ASSIMPMKLYSGIMCLIKSLIPAC---FNVVPHINGIESGILVAMADRYVAICYPLR	145
QY	135	HATVLTLPRTYKIGVAVVGAALMPLPYEIR-QLPFCRSNLSHSYCLHGVNKLACD	193
DB	146	HANIFHQVLVIQIGTMVNLAAITVAPCHVILICRQVFHTVYISHSYCHMAIVKIAA	205
QY	194	DIRNVYVGLIIVISAIGDSLISFSLYLTKVVLGL-TREAQAKFGCVSHCAVFI	252
DB	206	NVGVNRYKGLFVAFYVAGPFLFTLSYIQIFTVRPLPKRKAFAFNCAINHCIVFQ	265
QY	253	FYVPEIGLSNVHRSRKRDSPPLVITLNIYLVPPVLN	290
DB	266	FYLLAFSPFTHRGSH-----IPVYIH	288

##### RESULT 2

E45774 odorant receptor 8 - channel catfish

C:Species: Ictalurus punctatus (channel catfish)

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 26-Aug-1999

C:Accession: E45774

R:Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.

Cell 72, 657-666, 1993

A:Title: The family of genes encoding odorant receptors in the channel catfish.

A:Reference number: A45774; MIMD:93201590; PMID:7916654

A:Accession: E45774

A:Status: preliminary, not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-313 <NGA>  
 A:Experimental source: olfactory epithelium  
 A:Note: sequence extracted from NCBI backbone (NCBIP:127748)  
 C:Superfamily: olfactory receptor OR14  
 C:Keywords: olfaction; transmembrane protein

Query Match 29.4%; Score 477.5; DB 2; Length 313;  
 Best Local Similarity 34.4%; Pred. No. 6.7e-35;  
 Matches 106; Conservative 65; Mismatches 133; Indels 5; Gaps 4;

2 MDPNPNSSATYFLLIGLPGLEAOFWLAFLCSLYLAVNGNTIYIVTSHSHP 61  
 1 MAAVONISFTT-FTLPGHDGEMGPILSYLLMLSTSTNLTLYLISQRLASP 59  
 62 MYFLCMISGIDILISTSSMPKMLAFENSTTIOFDACILQMPAHSISGNESTVLLAM 121  
 60 MCLIGMAVVDLSMPICVPNMLISFLENMKGISLVGCLVGMFCIHGAGTQSTILLMN 119  
 122 ADRVAICHPRLHATVLTLPVTKIGVAAVKGALMAAPLFPVTKOLPFCRSNLSHSY 181  
 120 ADRFAICRPLPYOKYMGMPNLFEPVIRNLFETTVISNAGKLPFETNEIDHCY 179  
 182 CLHODVMKLACDDIRNVVYGLIYIISAIGDSLISFSYLLILKTVGLPREAQAKAG 241  
 180 CERMALVOLACDDISINNALGLITVFLITADPITITSTIYILVSL-RSKACLKAVN 238  
 242 TCVSHVCAVFIYVPFGLISVHRSKRDSPLP-VILANIYLVPPVLPVYGVKKE 300  
 239 TCITHIYVTSVLTFLALISYRI--RNFSSPSRVFLSTMYLIPSCNPFIYGVKKE 296  
 301 IGRILRL 308  
 297 IREQFLK 304

## RESULT 3

S29710  
 Olfactory receptor OR18 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 04-Sep-1998  
 C:Accession: S29710  
 R:Ramirez, K.; Krieger, J.; Strotmann, J.; Boehnke, I.; Kludick, S.; Baumstark, C.; Breer  
 Nature 361, 353-356, 1993  
 A:Title: Cloning and expression of odorant receptors.  
 A:Reference number: S29707; MUID:93149273; PMID:7678922  
 A:Accession: S29710  
 A:Molecule type: mRNA  
 A:Residues: 1-307 <RAM>  
 C:Superfamily: olfactory receptor OR14

Query Match 27.9%; Score 453; DB 2; Length 307;  
 Best Local Similarity 33.6%; Pred. No. 9.8e-33;  
 Matches 107; Conservative 64; Mismatches 125; Indels 22; Gaps 7;

7 GNESSATYFLLIGL---PGLERQFWLAFLCSLYLAVNGNTIYIVTSHSHP 63  
 2 GNNMTTEFTLGLTODPPGRALVYIF--LIIYVMGMNLTIVYVYASPSLSP 58  
 64 IFCMISGIDILISTSSMPKMLAFENSTTIOFDACILQMPAHSISGNESTVLLAM 123  
 59 FLIASLIDALFSTRALSKLADLITOKITSPRCKSQLETEHFGVDIVIIYANAY 118  
 124 DRVAICHPRLHATVLTLPVTKIGVAAVKGALMAAPLFPVTKOLPFCRSNLSHSY 183  
 119 DRVAICHPRLHATVLTLPVTKIGVAAVKGALMAAPLFPVTKOLPFCRSNLSHSY 178  
 184 HODVAKLADDDIRNVVYGLIYI--ISAIGDSLISFSYLLILKTVGLTREPQAKA 239  
 179 MSPFLVLAQD---TYFGLITVANGVNCIYIFLLIG-SYGIILRSKLTQSOGBERRA 234  
 240 FGVSHVCAVFIYVP--FGLISVHRSKRDSPLP-VILANIYLVPPVLPVYGVK 297

DB 235 ISTCSHILVYLFFPCFLFARPYNF-----PIDKCITYFTITPMLNPLITTLR 288  
 QY 298 TREIRORILRPHVATPA 315  
 DB 289 NSEIKSCMKKMKMHA 306

## RESULT 4

A6247  
 Olfactory receptor OR3 - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 26-Aug-1999  
 C:Accession: A6247  
 R:Net, P.; Hermans-Borgmeyer, I.; Attieres-Pin, H.; Beasley, L.; Dionne, V.E.; Rehm  
 Proc. Natl. Acad. Sci. U.S.A. 89, 8948-8952, 1992  
 A:Title: Spatial pattern of receptor expression in the olfactory epithelium.  
 A:Reference number: A6247; MUID:93028384; PMID:1384038  
 A:Accession: A6247  
 A:Status: preliminary, not compared with conceptual translation  
 A:Molecule type: nucleic acid  
 A:Residues: 1-312 <NEP>  
 A:Cross-references: GB:M64005; NID:9200153; PIDN:AAA39862.1; PID:9200154  
 C:Superfamily: olfactory receptor OR14

Query Match 27.1%; Score 440; DB 2; Length 312;  
 Best Local Similarity 34.6%; Pred. No. 1.4e-31;  
 Matches 113; Conservative 65; Mismatches 123; Indels 26; Gaps 11;

1 MMDPNSSATYFLLIGL---PGLERQFWLAFLCSLYLAVNGNTIYIVTSHSHP 57  
 1 MEYDSN---SSGTFILMGVSDHPHEIFEV---ILASITLVGNLTITLSRLAR 54  
 58 LHEPMTFLCMISGIDILISTSSMPKMLAFENSTTIOFDACILQMPAHSISGNESTV 117  
 55 LHPMTFPLNLSLDAFTTSVPMKMLMOPDKTISYGCCTVDLYELMGAFCIL 114  
 118 LLAMADRVAICHPRLHATVLTLPVTKIGVAAV--VGRALMAAPLFPVTKOLPFCRSN 175  
 115 LVMAADRVAICHPRLHATVLTLPVTKIGVAAV--VGRALMAAPLFPVTKOLPFCRSN 172  
 176 ILSHSCYCLHODVMKLACDDIRNV--VYGLIYIISAIGDSLISFSYLLILKTVGLT 232  
 173 KYDNFCEPAMKMLACGDTSLNENAVLNGCTFTYVPSVILV--SYCTIAAVKIRS 230  
 233 RBAQAKAFCTGVSHVCAVFIYVPFGLISVHRSKRDSPLP-VILANIYLVPPV 289  
 231 VEGRRKAFMTGVSHVCAVFIYVPFGLISVHRSKRDSPLP-VILANIYLVPPV 285  
 290 NPIYGVKTKERIKRILRPHVATPA 316  
 286 NPIYTLRNKRVGALGRLLGRGAS 312

## RESULT 5

123701  
 Olfactory receptor 114 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 26-Aug-1999  
 C:Accession: 123701  
 R:Buck, L.; Axel, R.  
 Cell 65, 175-187, 1991  
 A:Title: A novel multigene family may encode odorant receptors: a molecular basis for  
 A:Reference number: A23701; MUID:91191556; PMID:1840504  
 A:Accession: 123701  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-312 <BU>  
 A:Cross-references: GB:M64391; NID:9205843; PIDN:AAA1754.1; PID:9205844  
 C:Superfamily: olfactory receptor OR14  
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.8%; Score 434.5; DB 2; Length 312;  
 Best Local Similarity 33.5%; Pred. No. 4.4e-31;  
 Matches 105; Conservative 64; Mismatches 119; Indels 25; Gaps 7;

OY 8 NESAATYFLLGLPGLAEQFWLAFPLCSLYLAVLGNLTITTYREHSLHEPNTFLC 67  
 DB 5 NQVIVSGLLGLPGLAEQFWLAFPLCSLYLAVLGNLTITTYREHSLHEPNTFLC 64  
 OY 68 MLSGIDILISTSSMPKMLAFWRNSTIIOFDACLOQFAHSLSGMESTVLLAMAFDRY 127  
 DB 65 NLSFSDLCFSSTVMPKLOMNOQVPSISTYGCLOTFYFVWFGDMSEFLVYVAYDRY 124  
 OY 128 AICHPHATVTLPRVTKIGVAAYV-----RGALMAPLVPVTKOLPFCRSNLSHSY 181  
 DB 125 AICHPHATVTLPRVTKIGVAAYV-----RGALMAPLVPVTKOLPFCRSNLSHSY 178  
 OY 182 CLHODVNLACDDIRVN-----VYGLIYIISAIGDLSLSFSLILKTVLGL-TRBA 235  
 DB 179 CDISALTKLCSPIYVNEMLIYGLIITL-----PFLIYMSYVRIFFSILKFPSTIQD 233  
 OY 236 QARAFGCVSHCAVIFVFPYIGLSMVRHSKRSDSPVLITANIYLVPPVLPYVYG 295  
 DB 234 IYKVFSTCGSHLSVYTLFGYIGIYLCF--SGNNSYVKELAMAMVTVVPMNPFYIS 291  
 OY 296 VKTEIRORILRL 308  
 DB 292 LRNDMKRALIRV 304

RESULT 6  
 olfactory receptor HTRPC92 - human  
 JC5624  
 C/Species: Homo sapiens (man)  
 C/Date: 14-Oct-1997 #sequence\_revision 07-Nov-1997 #text\_change 20-Jun-2000  
 C/Accession: J05624; S58003  
 R/Vanderheghehen, P.; Schumann, S.; Vassart, G.; Parmentier, M.  
 Blochem. Biophys. Res. Commun. 237, 283-287, 1997  
 A/Title: Molecular cloning and chromosomal mapping of olfactory receptor genes expressed  
 A/Reference number: J05624; M0ID:97415789; PMID:9268701  
 A/Contents: Testis  
 A/Accession: J05624  
 A/Molecule type: mRNA  
 A/Residues: 1-319 <RAN>  
 A/Cross-references: GB:Y10530; NID:g7792017; PIDN:CAA71558.1; PID:g7792018  
 R/Vanderheghehen, P.; Schumann, S.; Vassart, G.; Parmentier, M.  
 Submitted to the EMBL Data Library, July 1995  
 A/Description: Male germ cells from several mammalian species express a specific repertoire  
 A/Reference number: S57995  
 A/Accession: S58003  
 A/Molecule type: mRNA  
 A/Residues: 126-282 <VAM>  
 A/Cross-references: EMBL:X89677; NID:g902337; PIDN:CAA61824.1; PID:g902338  
 C/Genetics:  
 A/Map position: 19p13.1  
 C/Function:  
 A/Description: Involved in control of sperm physiology  
 C/Superfamily: olfactory receptor OR14  
 C/Keywords: G protein-coupled receptor; transmembrane protein  
 F:26-48/Domain: transmembrane #status predicted <TM1>  
 F:38-79/Domain: transmembrane #status predicted <TM2>  
 F:101-120/Domain: transmembrane #status predicted <TM3>  
 F:140-164/Domain: transmembrane #status predicted <TM4>  
 F:197-218/Domain: transmembrane #status predicted <TM5>  
 F:237-260/Domain: transmembrane #status predicted <TM6>  
 F:272-292/Domain: transmembrane #status predicted <TM7>

Query Match 26.8%; Score 434.5; DB 2; Length 319;  
 Best Local Similarity 33.7%; Pred. No. 4.5e-31;  
 Matches 103; Conservative 70; Mismatches 118; Indels 15; Gaps 8;

OY 7 GNSSATYFLLGLPGLAEQFWLAFPLCSLYLAVLGNLTITTYREHSLHEPNTFLC 63  
 DB 4 GNTQVISEFLLGLPGLAEQFWLAFPLCSLYLAVLGNLTITTYREHSLHEPNTFLC 60

OY 64 IFCLMSGLDILISTSSMPKMLAFWRNSTIIOFDACLOQFAHSLSGMESTVLLAMAF 123  
 DB 61 FFLNLSFADLCVSTSTIPKMLMNTIQNKVITYIACLOMVFILRAGFNFLLSVAY 120  
 OY 124 DRYVACHPLRATVTLPRVTKIGVAAYVVGALMAPLVP-ETKOLPFCRSNLSHSYC 182  
 DB 121 DRYVACHPLR-HYVYVMPHLCGLVYASWMSALISLQILAMVRSFCYALRIPHEFC 179  
 OY 183 LHQDVNLACDDIRVN-----VYGLIYIISAIGDLSLSFSLILKTVLGL-TRBAQAKA 239  
 DB 180 ELNGVIOACSDSPFLNHVYFTVALGCGPLTGIL--YYSKIISSITHAISNAQKYKA 237  
 OY 240 FGTCVSHCAVIFVFPYIGLSMVRHSKRSDSPVLITANIYLVPPVLPYVYVYTK 299  
 DB 238 FSTCGSHLSVYSLFYGIVIGIYLCF--SANNSTYVETVAMVIVVPMNPFYISLNR 295  
 OY 300 EIRORILRL 308  
 DB 296 DIKRAL 301

RESULT 7  
 S29708  
 olfactory receptor OR12 - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 04-Sep-1998  
 C/Accession: S29708  
 R/Ramling, R.; Krieger, J.; Stroblmann, J.; Boekhoff, I.; Kubick, S.; Baumstark, C.;  
 Nature 361, 353-356, 1993  
 A/Title: Cloning and expression of odorant receptors.  
 A/Reference number: S29707; M0ID:93149273; PMID:7678922  
 A/Accession: S29708  
 A/Molecule type: mRNA  
 A/Residues: 1-312 <RAN>  
 C/Superfamily: olfactory receptor OR14

Query Match 26.7%; Score 433.5; DB 2; Length 312;  
 Best Local Similarity 32.0%; Pred. No. 5.4e-31;  
 Matches 99; Conservative 74; Mismatches 119; Indels 17; Gaps 6;

OY 8 NESAATYFLLGLPGLAEQFWLAF-PLCSLYLAVLGNLTITTYREHSLHEPNTFLC 65  
 DB 5 NQVIVSGLLGLP-IPPEHMLFYLITLANTYITIGNLTITLIDSNLHPMTLF 62  
 OY 66 LCMGIDILISTSSMPKMLAFWRNSTIIOFDACLOQFAHSLSGMESTVLLAMAFDR 125  
 DB 63 LSNLSFSDLCFSSTVMPKLOMNOQVPSISTYGCLOTFYFVWFGDMSEFLVYVAYDRY 122  
 OY 126 YVACHPLRATVTLPRVTKIGVAAYVVGALMAPLVPVTKOLPFCRSNLSHSYCLOH 185  
 DB 123 YVACHPLRATVTLPRVTKIGVAAYVVGALMAPLVPVTKOLPFCRSNLSHSYCLOH 182  
 OY 186 DVNKLACDDIRVN-----VYGLIYIISAIGDLSLSFSLILKTVLGL-TRBAQAKA 239  
 DB 183 ALNKLACDDIRVN-----VYGLIYIISAIGDLSLSFSLILKTVLGL-TRBAQAKA 237  
 OY 240 FGTCVSHCAVIFVFPYIGLSMVRHSKRSDSPVLITANIYLVPPVLPYVYVYTK 299  
 DB 238 FSTCGSHLSVYSLFYGIVIGIYLCF--SANNSTYVETVAMVIVVPMNPFYISLNR 295  
 OY 300 EIRORILRL 308  
 DB 296 DIKRAL 304

RESULT 8  
 G45774  
 odorant receptor 202 - channel catfish  
 C/Species: Ictalurus punctatus (channel catfish)  
 C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 04-Sep-1998  
 C/Accession: G45774  
 R/Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.



A:status: nucleic acid sequence not shown; not compared with conceptual translation  
 A:molecule type: mRNA  
 A:residues: 1-314 <RUC>  
 A:cross-references: GB:M64392; NID:q205845; PIDN:AAA1755.1; PID:q205846  
 C:superfamily: olfactory receptor OR14  
 C:keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.2%; Score 425.5; DB 2; Length 314;  
 Best Local Similarity 33.2%; Pred. No. 2.8e-30;  
 Matches 104; Conservative 70; Mismatches 114; Indels 25; Gaps 9;

8 NESATVFILIGLPGLEAQ--FWLAPLCSLYLANGLTIYVTEHSHLEPKYIF 65  
 DB 5 NQVYISQFLPLPISSEHOFVYALF--LSMTLVYLGMLITLITLHDSHLEPKYIF 62  
 OY 66 LCMISGIDILISTSMKPMALFENSTTIQDACLQMFALHSLSGMESTVLLAMFDR 125  
 DB 63 LSNLSPDLFFSVVTMKLQNNOSQVSPISFAGCLQQLFYLYKFALESFLVAMAYDR 122  
 OY 126 YVAICHPRLAATVLTLPRTKICVAAVNGAALM--APL-PVFIKOLPFCRSNITLSHY 181  
 DB 123 YVAICHPRLAATVLTLPRTKICVAAVNGAALM--APL-PVFIKOLPFCRSNITLSHY 178  
 OY 182 CLADQVAKLACDDIRVN----VYGLIVTIIAIGLDSILSPSYLLIKTVGL--TRFA 235  
 DB 179 CDSPLAKLSCDPRHVELYFVAGGLVYIPYV----LIVSYANVAVSILKVPESVKG 233  
 OY 236 QAAAFGCVSHVCAVFIFYVPIGLSMVHRFSKRDSPLPVIIANILVLPVNPITYG 295  
 DB 234 IHRIFSGSHLSVSLFETIIGLYLCP--SANNSTVKFEMAMVTVVTPMLNPITYS 291  
 OY 296 VKTEIRORIRL 308  
 DB 292 LRNDKMEALIRV 304

# RESULT 12

odorous receptor 3 - channel catfish  
 C:Species: Ictalurus punctatus (channel catfish)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 04-Sep-1998  
 C:Accession: H45774

R:Ngai, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A.  
 Cell 72, 657-666, 1993  
 A:title: The family of genes encoding odorant receptors in the channel catfish.  
 A:Reference number: H45774; MUID:93201590; PMID:7916654  
 A:Accession: H45774  
 A:status: preliminary; not compared with conceptual translation  
 A:molecule type: mRNA  
 A:Residues: 1-321 <NGA>  
 A:Experimental source: olfactory epithelium  
 A:Note: Sequence extracted from NCB1 backbone (NCBIP:127745)  
 C:superfamily: olfactory receptor OR14  
 C:keywords: olfaction; transmembrane protein

Query Match 26.2%; Score 424.5; DB 2; Length 321;  
 Best Local Similarity 32.7%; Pred. No. 3.5e-30;  
 Matches 102; Conservative 68; Mismatches 127; Indels 15; Gaps 6;

10 SSATV-----FILIGLPGLEAQFWLAPLCSLYLANGLTIYVTEHSHLEPKYI 64  
 DB 14 TMTFTIRPSPFYITGLYNIPHAKYTLF--LCFYTYVTFGLNSPFGITVILARSLHTAKYI 72  
 OY 65 FLMGSGIDILISTSMKPMALFENSTTIQDACLQMFALHSLSGMESTVLLAMFDR 124  
 DB 73 AVNMLASDLCGSSALIPKIDMLTFENOSISYEACISNMFYCFWTLQCLFLLALAYD 132  
 OY 125 RYVAICHPRLAATVLTLPRTKICVAAVNGAALMPLPVFIKOLPFCRSNITLSHY 184  
 DB 133 RLTAICHPRLAATVLTLPRTKICVAAVNGAALMPLPVFIKOLPFCRSNITLSHY 192  
 OY 185 ODVWLKACDDIRVN---VYGLIVTIIAIGLDSILSPSYLLIKTVGL--TRFA 240

DB 193 GPIYKACNDNTINSIMGNVCTAILPPLLIITIASYICGFALOKIARGV---EQYKAM 249  
 OY 241 GTCVSHVCAVFIFYVPIGLSMVHRFSKRDSPLPVIIANILVLPVNPITYG 300  
 DB 250 KTCSHLLVAMFYLPIISVTV--ALTTRIDTNIRIINTALQIFPPLNITITAKTEE 308  
 OY 301 IRQIRLRF-HV 311  
 DB 309 VMOAIRKLKRYHI 320

# RESULT 13

529711  
 olfactory factor OR37 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 04-Sep-1998  
 C:Accession: S29711  
 R:Ramng, K.; Krieger, J.; Strotmann, J.; Boehhoff, I.; Kudlick, S.; Baumstark, C.; I  
 Nature 361, 353-356, 1993  
 A:title: Cloning and expression of odorant receptors.  
 A:Reference number: S29707; MUID:93149273; PMID:7678922  
 A:Accession: S29711  
 A:molecule type: mRNA  
 A:Residues: 1-305 <RAM>  
 C:superfamily: olfactory receptor OR14

Query Match 26.0%; Score 422.5; DB 2; Length 305;  
 Best Local Similarity 32.8%; Pred. No. 5e-30;  
 Matches 101; Conservative 61; Mismatches 115; Indels 31; Gaps 5;

16 ILIGLPGLEAQFWLAPLCSLYLANGLTIYVTEHSHLEPKYIFLCMSGIDIL 75  
 DB 1 LILGSGPKTEILYFVLTAVLTIRHNGVLTIASIFDSHLTPMTFFGNLSFLDIC 60  
 OY 76 ISTSMKPMALFENSTTIQDACLQMFALHSLSGMESTVLLAMFDRVYALCHPLRH 135  
 DB 61 YTTSSVPSTIVSLSKRNISFGSGCTQMFVGFANGSTECILGMADRYALONPLRY 120  
 OY 136 ATVLTLPRTKI-----GVAAVNGAALMPLPVFIKOLPFCRSNITLSHY 187  
 DB 121 SVMSKEYVYMASASWFSGINSVYQTSIAM-----RLPFGNNVNIHFTEVLA 172  
 OY 188 MKLACDDIRVN---VYGLIVTIIAIGLDSILSPSYLLIKTVGL--TRFAOKAFGCVSH 246  
 DB 173 LKLCADISLNTVWVNMALFVLPILTFSTVLLITLIRNASAGRRKASTCSAH 232  
 OY 247 VCAVFIFYVPIGLSMVHRFSKRDSPL-----PVIIANILVLPVNPITYG 297  
 DB 233 LTVVVFETGTFISM-----YAKPKSQDLTGDKPQTSKIISLFGVGYTPMLNPITYSLR 287  
 OY 298 VKTEIRORI 305  
 DB 288 NKDVAAV 295

# RESULT 14

S29707  
 olfactory receptor OR5 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 26-Aug-1999  
 C:Accession: S29707; B37286  
 R:Ramng, K.; Krieger, J.; Strotmann, J.; Boehhoff, I.; Kudlick, S.; Baumstark, C.; I  
 Nature 361, 353-356, 1993  
 A:title: Cloning and expression of odorant receptors.  
 A:Reference number: S29707; MUID:93149273; PMID:7678922  
 A:Accession: S29707  
 A:molecule type: mRNA  
 A:Residues: 1-314 <RAM>  
 R:Buck, L.; Axel, R.  
 Cell 65, 175-187, 1991  
 A:title: A novel multigene family may encode odorant receptors: a molecular basis for  
 A:Reference number: A23701; MUID:91191556; PMID:1840504  
 A:Accession: B37286

A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 193-236 <BUC>  
 A:Cross-references: GB:M64375; NID:g205811; PIDN:AAA41738.1; PID:g205812  
 C:Superfamily: olfactory receptor OR14  
 C:Keywords: G protein-coupled receptor; membrane protein

Query Match 25.9%; Score 420.5; DB 2; Length 314;

Best Local Similarity 34.1%; Pred. No. 7.8e-30; Mismatches 119; Indels 15; Gaps 7;

Matches 103; Conservative 65; Mismatches 119; Indels 15; Gaps 7;

8 NESATYFLLGLGLEAQAQ--FMIAFPLCSLYLAVALGNLTIIYIVREHSLHEPMYIF 65

5 NGYISQPLGLGLPIPHGHQHTFALF--LSMYLFTIIGNLIIIIILDSLHPMYIF 62

66 LCMISGIDILISTSSMPFMAIAIFWNSSTTIOFACLLQFAIHSLSGMESTVLLAAEDR 125

63 LSNLSFSDLCFSSVYMPKILQNMOSQVPSIPYAGCLSLQYFPLFGDLGNFLVMAAYDR 122

126 VYATCHPIRHAATVTLPRVTIGVAAYVRGALM--APL-PVFTRKQLPFCSSNIIISHY 181

123 VYATCFPLHYSINS---PKICVSLVLSWLTTFHMLATLILMARLSFCEDNVIPIHF 178

182 CLHODVMTACDDIRVNVVYGLIYISAIGLDSLISFSYLLIKTVLGL-TREAQAKAF 240

179 CDMSHLLACSDIRVNEVYIFIVSLPLVLPFALIIISYVAIVSSILKVPSSQGIYKAF 238

241 GTCVSHVCAVEFFVYFPIGLSMVHRFSKRSDPLPVIIANIYLLVPPVLPVYGVYKRE 300

239 SSCGSHLSVSLFVGTIVLPYLCP--SSNNSVYKQVMSLMYTLVTPMLNPFYISLRND 296

301 IR 302

297 IR 298

RESULT 15

513356

olfactory receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: S51356; S47014

R:Gat. U.; Nekrasova, E.; Lancel, D.; Natochin, M.

Eur. J. Biochem. 225, 1157-1168, 1994

A:Title: Olfactory receptor proteins. Expression, characterization and partial purification

A:Reference number: S51356; MUID:95045546; PMID:7957207

A:Accession: S51356

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-309 <GAT>

A:Cross-references: EMBL:X80671; NID:g517365; PIDN:CAA56697.1; PID:g517366

R:Gat. U.; Nekrasova, E.; Lancel, D.; Natochin, M.

submitted to the EMBL Data Library, July 1994

A:Description: Olfactory receptor proteins: expression, characterization and partial purification

A:Reference number: S47014

A:Accession: S47014

QY 127 VAICRPLRHAATVTLPRVTIGV-----AAVVRGALMAFLPVFTRKQLPFCSSNII 177

DB 125 VAICRPLRHAATVTLPRVTIGV-----AAVVRGALMAFLPVFTRKQLPFCSSNII 175

QY 178 SHSYCLHODVMTACDDIRVNVVYGLIYISAIG--LDSILISFSYLLIKTVLGL-TRE 234

DB 176 SHYFCDALPLKTLACSNHMLNEL--LIFLIGLNTLVPLIAVAISVYFICSLIRRSSE 233

QY 235 AOKAFGTCVSHVCAVEFFY--VPFGLSMVHRFSKRSDPLPVIIANIYLLVPPVLPV 292

DB 234 GRKAFGTCVSHVCAVEFFY--VPFGLSMVHRFSKRSDPLPVIIANIYLLVPPVLPV 289

QY 293 VYGVKTRKQLPFCSSNIIISHY 307

DB 290 IYSLRNDVYKALGR 304

Search completed: March 26, 2003, 09:57:05

Job time : 48 secs

Query Match 25.8%; Score 418.5; DB 1; Length 309;

Best Local Similarity 33.0%; Pred. No. 1.1e-29; Mismatches 104; Conservative 63; Mismatches 119; Indels 29; Gaps 8;

7 GNEASATFLLGLGLEAQAQ--FMIAFPLCSLYLAVALGNLTIIYIVREHSLHEPMYIFL 66

5 GNEASATFLLGLGLEAQAQ--FMIAFPLCSLYLAVALGNLTIIYIVREHSLHEPMYIFL 64

67 CMLSGIDILISTSSMPFMAIAIFWNSSTTIOFACLLQFAIHSLSGMESTVLLAAEDR 126

65 SLSFVSDLCFSSVYMPKILQNMOSQVPSIPYAGCLSLQYFPLFGDLGNFLVMAAYDR 124

GenCore version 5.1.4.p5\_4578  
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OM protein - protein search, using sw model

Run on: March 26, 2003, 09:48:21 ; Search time 25 seconds

(without alignments)  
527.379 Million cell updates/sec

Title: US-09-966-459a-2

Perfect score: 1623

Sequence: 1 MVDNGNENSSATYFLLGL.....KEIRQRILRLFHVATNASEP 318

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	983	60.6	320	1	OXE2_HUMAN
2	981	60.4	320	1	OXE2_RAT
3	872.5	53.8	312	1	OX12_HUMAN
4	810.5	49.9	314	1	OX11_HUMAN
5	796.5	49.1	318	1	OXD1_HUMAN
6	778.5	48.0	315	1	OXM1_HUMAN
7	763	47.0	317	1	OXR2_HUMAN
8	755	46.5	312	1	OYA1_HUMAN
9	728.5	44.9	312	1	OXB2_HUMAN
10	708	43.6	313	1	OYE6_HUMAN
11	633	39.0	310	1	OXB4_HUMAN
12	468	28.8	319	1	OZS2_HUMAN
13	440	27.1	312	1	OL15_MOUSE
14	435.5	26.8	314	1	OYF1_HUMAN
15	434.5	26.8	312	1	OLE4_RAT
16	434.5	26.6	319	1	O7A5_HUMAN
17	432.5	26.6	312	1	O2C1_HUMAN
18	431.5	26.6	310	1	OLE0_RAT
19	431	26.6	314	1	O1E1_HUMAN
20	430	26.6	323	1	O1E2_HUMAN
21	428.5	26.4	311	1	OA42_HUMAN
22	428.5	26.4	311	1	O6B1_HUMAN
23	428	26.4	317	1	OLF3_CANFA
24	427.5	26.3	312	1	O1F1_HUMAN
25	426.5	26.3	315	1	OB41_HUMAN
26	425.5	26.2	314	1	OLF1_RAT
27	425	26.2	317	1	OA45_HUMAN
28	423.5	26.1	321	1	O5V1_HUMAN
29	422.5	26.0	320	1	O7C1_HUMAN
30	421	25.9	317	1	O2F1_HUMAN
31	420.5	25.9	312	1	OLF6_CHICK
32	420.5	25.9	313	1	O1C1_HUMAN
33	420.5	25.9	314	1	OAA3_HUMAN

34	418	25.8	311	1	O5P3_HUMAN	08W294 homo sapien
35	415.5	25.6	312	1	OLF4_CHICK	P37070 gallus gall
36	413.5	25.5	311	1	O2J3_HUMAN	O76001 homo sapien
37	413	25.4	312	1	O1D2_HUMAN	P34987 homo sapien
38	412.5	25.4	318	1	OLF1_CHICK	P37067 gallus gall
39	411.5	25.4	311	1	O8B8_HUMAN	O15620 homo sapien
40	411	25.3	311	1	OLF1_CANFA	O95154 canis faml
41	411	25.3	313	1	OLF2_CANFA	P30955 canis faml
42	411	25.3	318	1	O4H1_HUMAN	O9Y488 homo sapien
43	410	25.3	309	1	O5B2_HUMAN	O96408 homo sapien
44	409.5	25.2	313	1	O2B6_HUMAN	P58173 homo sapien
45	409.5	25.2	313	1	OLF5_RAT	P23266 rattus norv

## ALIGNMENTS

RESULT 1  
ID OXE2\_HUMAN STANDARD; PRT; 320 AA.  
AC 09H255;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Olfactory receptor 51E2 (Prostate specific G-protein coupled receptor)  
DE (HPRJ).  
GN OR51E2 OR PSGR.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21002538; PubMed=11118034;  
RA Xu L.L., Stackhouse B.G., Florence K., Zhang W., Shanmugam N.,  
RA Sesterhenn I.A., You Z., Srikantan V., Augustus M., Roschke V.,  
RA Carter K., McLeod D.G., Moui J.W., Soppet D., Srivastava S.;  
RT "PSGR", a novel prostate-specific gene with homology to a G  
RT protein-coupled receptor, is overexpressed in prostate cancer.";  
RL Cancer Res. 60:6568-6572(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21564169; PubMed=11707321;  
RA Yuan T.-T., Toy P., McClary J.A., Lin R.J., Miyamoto N.G.,  
RA Kretschmer P.J.;  
RT "Cloning and genetic characterization of an evolutionarily conserved  
RT human olfactory receptor that is differentially expressed across  
RT species.";  
RL Gene 278:41-51(2001).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX Strausberg R.;  
RT Tissue-Prostate;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
CC - FUNCTION: PUTATIVE ODORANT RECEPTOR.  
CC - SUBCELLULAR LOCATION: Integral membrane protein.  
CC - TISSUE SPECIFICITY: EXCLUSIVELY EXPRESSED IN THE PROSTATE.  
CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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CC EMBL: AF311306; AAG40776.1; -
DR EMBL: AF369708; AAK38728.1; -
DR EMBL: AF039942; AAK37550.1; -
DR EMBL: BC020768; AAK20768.1; -
DR Genew: HGNC:15195; ORS152.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; transmembrane; glycoprotein.
FT DOMAIN 1 23
FT TRANSMEM 24 48
FT DOMAIN 49 59
FT TRANSMEM 60 84
FT DOMAIN 85 100
FT TRANSMEM 101 119
FT DOMAIN 120 142
FT TRANSMEM 143 162
FT DOMAIN 163 197
FT TRANSMEM 198 221
FT DOMAIN 222 235
FT TRANSMEM 236 260
FT TRANSMEM 261 269
FT TRANSMEM 270 292
FT DOMAIN 293 320
FT DISULFID 96 178
FT CARBOHYD 5 5
SQ SEQUENCE 320 AA; 35492 MW; 03582CC2AAB6E2C6 CRC64;

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Query Match Best Local Similarity 59.8%; Score 983; DB 1; Length 320;

Matches 183; Conservative 54; Mismatches 67; Indels 2; Gaps 2;

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OY 8 NESSATYFLILGPGLEAOFMLAPLCSLYLAVGLNTLIYVTERSLHEPMTIFLC 67
DB 5 NEFHAT-FVLIGIPGLEKAFHFWGFPFLSMYVAMGNCIVAYIVTERSLHAPMTIFLC 63
OY 68 MNSGDIILSTSSMPKMLAIFWNSITTOFDACILOMFAHISGSESVLLAMADRY 127
DB 64 MLAADLALSTSTMPKILALFWDSREITFDACILOMFAHISGSESVLLAMADRY 123
OY 128 AICHPLEHATVTLPRFKIGVAAVRGAALAPLFPVKOLPFCRSNLTISYCYLHOPV 187
DB 124 AICHPLEHATVTLPRFKIGVAAVRGAALAPLFPVKOLPFCRSNLTISYCYLHOPV 183
OY 188 MLIACDDIRNVVYGLVITISAIGLDSLISFSYLLIKTVGL-TREAQAKFGTCVSH 246
DB 184 MLIACDDIRNVVYGLVITISAIGLDSLISFSYLLIKTVGL-TREAQAKFGTCVSH 243
OY 247 VCAVLEFYVPIGLSNVHRSKRSDPLPYLLANTYLLVPVLPVYGVTKREIKRQL 306
DB 244 IGVYLAFTVPLIGLSVHRSKRLDPIYVAVGDIYLLPVPINPIYAKTKQIRTVL 303
OY 307 RLEHVA 312
DB 304 AMFKIS 309

```

## RESULT 2

ID OXE2\_RAT STANDARD; PRT; 320 AA.

```

AC 088628;
DB 16-OCT-2001 (Rel. 40; Created)
DB 16-OCT-2001 (Rel. 40; Last sequence update)
DB 16-OCT-2001 (Rel. 40; Last annotation update)
DE Olfactory receptor 5122 (G-protein coupled receptor RALc).
GN ORS152.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99131082; PubMed=9932290;
RA Raming K., Konzelmann S., Breer H.;
RT Identification of a novel G-protein coupled receptor expressed in
RT distinct brain regions and a defined olfactory zone.;
RL Recept. Channels 6:141-151(1998).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN SOME AREAS OF THE BRAIN AND
CC IN THE OLFACTORY EPITHELIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@sdb.ch).
CC
CC EMBL: AF079864; AAD12761.1; -
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR PROSITE: PS0262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; transmembrane; glycoprotein.
FT DOMAIN 1 23
FT TRANSMEM 24 48
FT DOMAIN 49 59
FT TRANSMEM 60 84
FT DOMAIN 85 94
FT TRANSMEM 95 119
FT DOMAIN 120 138
FT TRANSMEM 139 162
FT TRANSMEM 163 197
FT TRANSMEM 198 221
FT DOMAIN 222 235
FT TRANSMEM 236 260
FT DOMAIN 261 269
FT TRANSMEM 270 292
FT DOMAIN 293 320
FT DISULFID 96 178
FT CARBOHYD 5 5
SQ SEQUENCE 320 AA; 35505 MW; E7F78F5FDSBP94 CRC64;

```

Query Match Best Local Similarity 60.4%; Score 981; DB 1; Length 320;

Matches 183; Conservative 52; Mismatches 69; Indels 2; Gaps 2;

```

OY 8 NESSATYFLILGPGLEAOFMLAPLCSLYLAVGLNTLIYVTERSLHEPMTIFLC 67
DB 5 NEFHAT-FVLIGIPGLEKAFHFWGFPFLSMYVAMGNCIVAYIVTERSLHAPMTIFLC 63
OY 68 MNSGDIILSTSSMPKMLAIFWNSITTOFDACILOMFAHISGSESVLLAMADRY 127
DB 64 MLAADLALSTSTMPKILALFWDSREITFDACILOMFAHISGSESVLLAMADRY 123
OY 128 AICHPLEHATVTLPRFKIGVAAVRGAALAPLFPVKOLPFCRSNLTISYCYLHOPV 187
DB 124 AICHPLEHATVTLPRFKIGVAAVRGAALAPLFPVKOLPFCRSNLTISYCYLHOPV 183
OY 188 MLIACDDIRNVVYGLVITISAIGLDSLISFSYLLIKTVGL-TREAQAKFGTCVSH 246
DB 184 MLIACDDIRNVVYGLVITISAIGLDSLISFSYLLIKTVGL-TREAQAKFGTCVSH 243
OY 247 VCAVLEFYVPIGLSNVHRSKRSDPLPYLLANTYLLVPVLPVYGVTKREIKRQL 306
DB 244 IGVYLAFTVPLIGLSVHRSKRLDPIYVAVGDIYLLPVPINPIYAKTKQIRTVL 303
OY 307 RLEHVA 312
DB 304 AMFKIS 309

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DB 304 AMFKIS 309

RESULT 3

OX12\_HUMAN STANDARD; PRT; 312 AA.

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

Olfactory receptor 5112 (HORS/beta12).

OR5112.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI\_TaxID=9606;

SEQUENCE FROM N.A.

MEDLINE=20570519; PubMed=11121057;

Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell C.M., Felsenfeld G., Groudine M., Hardison R.;

\*Comparative structural and functional analysis of the olfactory receptor genes flanking the human and mouse beta-globin gene clusters.\*

Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).

-1- FUNCTION: PUTATIVE ODORANT RECEPTOR.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

-----

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-----

EMBL: AF137396; AAC41678.1;

InterPro: IPR000276; GPCR\_Rhodopsn.

DR Pfam: PF00001; 7tm.1. 1.

DR PRINTS: PR00237; GPCR\_Rhodopsn.

DR PROSITE: PS00237; G\_PROTEIN\_REC\_P1\_1; 1.

DR PROSITE: PS0262; G\_PROTEIN\_REC\_P1\_2; 1.

KW G-protein coupled receptor; Transmembrane; Glycoprotein;

KW Multigene family; Olfaction.

FT DOMAIN 1 25

FT TRANSMEM 26 49

FT DOMAIN 50 57

FT TRANSMEM 58 79

FT DOMAIN 80 100

FT TRANSMEM 101 120

FT DOMAIN 121 139

FT TRANSMEM 140 158

FT DOMAIN 159 195

FT TRANSMEM 196 219

FT DOMAIN 220 236

FT TRANSMEM 237 259

FT DOMAIN 260 268

FT TRANSMEM 275 294

FT DISULFID 295 312

FT CARBOHD 97 189

FT SEQUENCE 312 AA; 35002 MW; F17CD16C95FD1AF6 CRC64;

Query Match 53.8%; Score 872.5; DB 1; Length 312;

Best Local Similarity 53.9%; Pred. No. 3.4e-59;

Matches 164; Conservative 50; Mismatches 89; Indels 1; Gaps 1;

DB 8 NTSATPFLTGLPGLLEAGFLAPPLCLSLVAVGNFTIYIYRTESLHPMTIFLC 67

DB 5 NTHPAFLFLTSLIPGLSSHSLSGPLCVAVAGNVTIQAARVERPSLHPMTIFLS 64

QY 68 MLSGDILISTSMKMLAIFWNSTTIOFDACLLQMFALHSLGMSVLLAMADRYV 127

DB 65 MTSFQVAISMATLPYLRFPCLANRITFDACLIQMLTFHFSMMSGILLMSFGRYV 124

QY 128 AICHPLEHATVTLPRYTKGVAAYVGAALAPLPYFIKQDPGCSNITSHSYCLHODY 187

DB 125 AICDPLRYATVATLTVETVAAGLGAARSFTPLPLRLRPLRDLCSNVTLSHSYCLPDM 184

QY 188 MKIACGDIRNVVYGLVITISAIIGDLSLISFSLVILTKTVIGL-LTRERQAKRGCVSH 246

DB 185 MKIACADISNISTYGLFVLTSTFGMDLFTFLSVLILSVMTASKEERKALNTCVSH 244

QY 247 VCAVFTFYVPEIGLSVWHRFSKRSDPLPYLIANYLVLPVLPVYGVKTEIRORIL 306

DB 245 ILAVLAVFYVMIGVSVYHRGKAVPCIVHLYMENVTLFVPPVLPVLSAKTEIRAIRF 304

QY 307 RLPH 310

DB 305 RMPH 308

RESULT 4

OX12\_HUMAN STANDARD; PRT; 314 AA.

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Olfactory receptor 5111 (HORS/beta11).

OR5111.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI\_TaxID=9606;

SEQUENCE FROM N.A.

MEDLINE=20570519; PubMed=11121057;

Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell C.M., Felsenfeld G., Groudine M., Hardison R.;

\*Comparative structural and functional analysis of the olfactory receptor genes flanking the human and mouse beta-globin gene clusters.\*

Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).

-1- FUNCTION: PUTATIVE ODORANT RECEPTOR.

-1- SUBCELLULAR LOCATION: Integral membrane protein.

-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

-----

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-----

EMBL: AF137396; AAC41679.1;

InterPro: IPR000276; GPCR\_Rhodopsn.

DR Pfam: PF00001; 7tm.1. 1.

DR PRINTS: PR00237; GPCR\_Rhodopsn.

DR PROSITE: PS00237; G\_PROTEIN\_REC\_P1\_1; 1.

DR PROSITE: PS0262; G\_PROTEIN\_REC\_P1\_2; 1.

KW G-protein coupled receptor; Transmembrane;

KW Multigene family; Olfaction.

FT DOMAIN 1 27

FT TRANSMEM 28 51

FT DOMAIN 52 59

FT TRANSMEM 60 81

FT DOMAIN 82 102

FT TRANSMEM 103 122

FT DOMAIN 123 141

FT TRANSMEM 142 160

FT DOMAIN 161 197

FT TRANSMEM 198 221

FT DOMAIN 222 238

QY 222

```

FF TRANSSEM      239    261    6 (POTENTIAL).
FF DOMAIN        262    270    EXTRACELLULAR (POTENTIAL).
FF TRANSEM      277    296    7 (POTENTIAL).
FF DOMAIN        297    314    CYTOPLASMIC (POTENTIAL).
FT DISULFID     99    191    BY SIMILARITY.
SQ SEQUENCE     314 AA; 35483 MW; 08B40AD79CB94911 CRC64;

Query Match          49.9%; Score 810.5; DB 1; Length 314;
Best Local Similarity 48.7%; Pred. No. 1,7e-54;
Matches 151; Conservative 65; Mismatches 93; Indels 1; Gaps 1;

OY 2 WVDPNGNSSATYPIYLGLPGLEAEQWLAAPLCSLYLIAVGLNLIYYIVRTEHSHEP 61
   : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MLGNGCPFPQATQLGTGIPGIQTGLFWVALIFCLIMISITVGNSILTIVFEWEPALHQ 60
   : ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 62 MTIPLCMSCGIDILISTSMRMLAIFFNSTTIOFDACLQMRAHSLSGMESTVLAM 121
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 MYFLSMALNDLDIGSFSTLPVTISTFCFNNHNFAFNCLVOMEFIRHTSPMESGILLAM 120
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 122 AEDRVVAICHPLRHFTVTLTPVRKIGAAVAVRGAAALMAPLVFKOLKOPPCRSNIHSY 181
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 SLDNRVACITPKRYRTVLTNNRLIAMGLIKSTTLPPEPVVKRIKPFCKGVNLHSHY 180
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 182 CLHDPMIAACDDINNVVYGLVIITSAIGDLSLISFSYLLIKTVLG-LTREAOAKAF 240
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 CHAPLMIAVAGSDIHVNNYIGLVIIIFYGMDSTFILLSYALLLRAMLVIISQERLAL 240
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 241 CTCVSHCAVFIFYPPFIGLSKMHFRSRRDSPLEYIILANILYLVPLVNPVIVGYKTK 300
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 NTCMSHCIAVALFYPIILAVISMIRFRKSPAPVVHMANSYLFVPMLNDPIIVSYKTK 300
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

OY 301 INORILRLPH 310
Db 301 INKGILKEFH 310
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 5
OYDL_HUMAN
ID OYDL_HUMAN STANDARD; PRF: 318 AA.
AC Q9RH46;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 52D1 (HOR5/beta14).
GN OR52D1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-20570519; PubMed-11121057;
RA Bulger.M., Bender.M.A., van Doornick J.H., Wertman B., Farrell C.N.,
RA Felsenfeld.G., Grundine M., Hardison R.;
RT *Comparative structural and functional analysis of the olfactory
RT receptor genes flanking the human and mouse beta-globin gene
RT clusters.;
RT Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).
RL -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
EMBL AF137396; AACGA1676.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
```

DR	PRINTS: PRO0237; GPCRHHODPSN.
DR	PROSITE: PS00237; G-PROTEIN RECEPTOR FL1; 1.
DR	PROSITE: PS0262; G-PROTEIN RECEPTOR FL2; 1.
KM	G-protein coupled receptor; Transmembrane; Glycoprotein;
KW	Multi-gene family; Olfaction.
FT	DOMAIN 1 28
FT	TRANSMEM 29 52
FT	DOMAIN 53 60
FT	TRANSMEM 61 82
FT	DOMAIN 83 103
FT	TRANSMEM 104 123
FT	DOMAIN 124 142
FT	TRANSMEM 143 161
FT	DOMAIN 162 198
FT	TRANSMEM 199 222
FT	DOMAIN 223 239
FT	TRANSMEM 240 262
FT	DOMAIN 263 272
FT	TRANSMEM 279 298
FT	DOMAIN 299 318
FT	DISULFID 100 192
FT	CARBOHYD 5 5
SO	SEQUENCE 318 AA; 35121 MW; 178968087D613CB2 CRC64;
Query Match	49.1%; Score 796.5; DB 1; Length 318;
Best Local Similarity	46.5%; Pred. No. 1.9e-53;
Matches 146; Conservative 70; Mismatches 93; Indels 5; Gaps	
OY	2 MVDPN--GNESAAVFILGLPGLEDAQFWALPFCISLYLAVLGNLTITVYRTSHSLH 59
DB	1 MDSNLSNHLPEDFE--LTGIPGLRAHFHWIAPPCANTVALVAGNALIIVADNMLH 59
OY	60 ERMVFICMLSGIDILISSMPKMLATFWMSTTIQDADCLQWFAHSLSGMSTVLL 119
DB	60 AEMVFICILSTFDALSTSTVPKMLATLMLAGEISFGGALQMFVCHSTALSSILL 119
OY	120 AMAFRVYAICPHLRAVTLTPRTYKIGVAVNGAALMLAPLPIFKOLPCRSNIIISH 179
DB	120 AMAFRVYAICNPLRYTITLNAVYGRIGFVGLFSAVNPSPFILLRLRPGCGRWYH 179
OY	180 STCLHODVAKLACDDIRVNVYGLIVITSAIGLSLISFSTYLLIKTVYGL--TREDAQK 238
DB	180 TYCEHNGIARLACANITVNIYGLTVALLAMGLDSILLTASIGFIIHVFHPSHDAQK 239
OY	239 AFGCVSHVCAFTITVYVPIGLSNHRSKR--DSPLVILANTITLVDPVLPNPVYGVK 297
DB	240 ALSTGSHIGILVYIYPAFSEFLTHRGHNEVPRAVHFIAMLVLPVLPNPILYGAR 299
OY	298 TREIRORILRPHV 311
DB	300 TREIRSLKLTLHL 313
RESULT 6	
OXML_HUMAN	
ID	OXML_HUMAN STANDARD: PRF: 315 AA.
AC	Q9H341;
DF	15-JUN-2002 (Rel. 41, Created)
DF	15-JUN-2002 (Rel. 41, Last sequence update)
DF	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Olfactory receptor 51M1 (HORS/beta7).
GN	OR51M1.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEJLIN-20570519; PubMed=11121057;
RA	Bulger M., Bender M.A., van Dornick J.H., Wertman B., Farrell C.M.,
RT	Reisenfeld G., Groudine M., Hardison R.
RT	"Comparative structural and functional analysis of the olfactory
RT	receptor genes flanking the human and mouse beta-globin gene

```

RT clusters.
RL Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF137396; AAC1681.1; ALT. INIT.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSN.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 26 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 27 50 1 (POTENTIAL).
FT DOMAIN 51 58 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 59 80 2 (POTENTIAL).
FT DOMAIN 81 101 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 102 121 3 (POTENTIAL).
FT DOMAIN 122 140 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 141 159 4 (POTENTIAL).
FT DOMAIN 160 196 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 197 220 5 (POTENTIAL).
FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 238 260 6 (POTENTIAL).
FT DOMAIN 261 275 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 276 295 7 (POTENTIAL).
FT DOMAIN 296 315 CYTOPLASMIC (POTENTIAL).
FT DISULFID 98 190 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 315 AA; 35462 MW; DC19D2F5456D2005 CRC64;

Query Match 48.0%; Score 778.5; DB 1; Length 315;
Best Local Similarity 47.8%; Pred. No. 4,4e-52;
Matches 141; Conservative 64; Mismatches 89; Indels 1; Gaps 1;

QY 15 FILGLGLEAEQWLAFLPCLSLYLAIVGNLTIYIVRTHSHHEMYIFLCMLSGIDI 74
DB 13 FYLSPFGLGSLKIMFIPIFFFMVAISGNCFTLIITKIPRLATPMYILSLATLDTL 72
QY 75 LISTSSPKMLAIFWPNSTTIOFDACLOMFALHSLSGMESTVILAMAFDRVAICHLR 134
DB 73 GLCVSTIPTMGITWPNSSQIYFACIOIOMFCHISFSPMESTVILAMSFDFVAICHLR 132
QY 135 HATVLTLPRTKIGVAANVRGAALMADLPVFIKQLPFCRSNIILSHSYCLHODVKNLACD 194
DB 133 YSVIITGQVVRAGLIYIFRGPAVITIPYILLLKAFPGCVSVLSHSCPLHQEVIQLACTD 192
QY 195 IRVNVVGLIYIISAIGDSLISFSYLLIKTYLGL-TREAQAKAGTCVSHCAVPIF 253
DB 193 TTFNNKLGIAVWVETVMDLYLALSTGLILHTVAGLASEBQRRAROTCAHRCAYLVE 252
QY 254 YVPEIGLSVHRESKRDSPPLVILANITYLIVPVANPIYGVATKTEIRORIL 308
DB 253 FVPAMGLSLVHRGKAPPAIHILMANVYLFVPMALNPIITISIKTEIHRATIKL 307

RESULT 7
ID QYB2_HUMAN STANDARD; PRT; 317 AA.
AC Q96RD2:
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

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DE Olfactory receptor 5282.
GN OR5282.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE OF 70-287 FROM N.A.
RA Fuchs T., Molecova B., Linhart C., Sharan R., Khan M., Herwig R.,
RA Simulovich D., Eikon R., Steinfach M., O'Brien J.K., Radcliff U.,
RA Lénvácz H., Olander Z., Glusman G., Lancet D., Shamir R.;
RA "DEFOC: a practical scheme for deciphering families of genes."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL: AF399505; AK94990.1;
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 28 51 1 (POTENTIAL).
FT DOMAIN 52 59 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 60 81 2 (POTENTIAL).
FT DOMAIN 82 102 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 103 122 3 (POTENTIAL).
FT DOMAIN 123 141 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 142 160 4 (POTENTIAL).
FT DOMAIN 161 197 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 198 221 5 (POTENTIAL).
FT DOMAIN 222 238 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 239 261 6 (POTENTIAL).
FT DOMAIN 262 276 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 277 296 7 (POTENTIAL).
FT DOMAIN 297 317 CYTOPLASMIC (POTENTIAL).
FT DISULFID 99 191 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 317 AA; 35642 MW; DB17DB8791F85E21 CRC64;

Query Match 47.0%; Score 763; DB 1; Length 317;
Best Local Similarity 46.2%; Pred. No. 6.5e-51;
Matches 148; Conservative 57; Mismatches 94; Indels 2; Gaps 2;

QY 15 FILGLGLEAEQWLAFLPCLSLYLAIVGNLTIYIVRTHSHHEMYIFLCMLSGIDI 74
DB 14 FYLSPFGLGSLKIMFIPIFFFMVAISGNCFTLIITKIPRLATPMYILSLATLDTL 73
QY 75 LISTSSPKMLAIFWPNSTTIOFDACLOMFALHSLSGMESTVILAMAFDRVAICHLR 134
DB 74 LLSSTVYKALAIEMIAHNIATFDACVQGFVHMEGESAIIILAMAFDFVAICHLR 133
QY 135 HATVLTLPRTKIGVAANVRGAALMADLPVFIKQLPFCRSNIILSHSYCLHODVKNLACD 194
DB 134 YTVVLTWVGRILAVTRTSCFIPIFLLKRLPCLTINIVPSTCEHIGVANLACD 193
QY 195 IRVNVVGLIYIISAIGDSLISFSYLLIKTYLGL-TREAQAKAGTCVSHCAVPIF 253
DB 194 ITVINWGFSPPIYAVILDLIIVSYLLIARFRLPSQARHKAALSTGSHLCVILMF 253
QY 254 YVPEIGLSVHRESKRDSPPLVILANITYLIVPVANPIYGVATKTEIRORIL-RLFVA 312
DB 254 YVPSFTLLTHTHFGKNIPQHVHILANLYAVVPMALNPIYGVATKTRQIREGVAHREFDIK 313

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CC EMBL: AF137396; AAD29425.2; -  
DR EMBL: AF399503; AAK94988.1; -  
DR Genew; HGNC:14703; ORS1B2.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm.1.1.  
DR PRINTS; PS00237; GPCR\_RHODOPSIN.  
DR PROSITE; PS00237; G\_PROTEIN\_RECP.F1.1; 1.  
DR PROSITE; PS00262; G\_PROTEIN\_RECP.F1.2; 1.  
DR G-protein coupled receptor; Transmembrane; glycoprotein;  
KW Multigene family; Olfaction.  
FT DOMAIN 1 23 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 48 47 1 (POTENTIAL).  
FT DOMAIN 56 55 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 77 77 2 (POTENTIAL).  
FT DOMAIN 98 98 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 118 118 3 (POTENTIAL).  
FT DOMAIN 119 137 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 138 156 4 (POTENTIAL).  
FT DOMAIN 157 193 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 194 217 5 (POTENTIAL).  
FT DOMAIN 218 234 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 235 257 6 (POTENTIAL).  
FT DOMAIN 266 266 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 273 292 7 (POTENTIAL).  
FT TRANSMEM 293 312 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 95 187 BY STIMILARITY.  
FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 312 AA; 35513 MW; 0DA1160267778BDD CRC64;  
  
Query Match 44.9%; Score 728.5; DB 1; Length 312;  
Best Local Similarity 44.1%; Pred. No. 2,6e-48;  
Matches 132; Conservative 76; Mismatches 90; Indels 1; Gaps 1;  
  
QY 11 SATYFLLGLPGLEAOFWLAFLPLCSLYLAIVAGNTTIIVTSHLEPNTFLCMS 70  
DB 6 TAAPEFLTGFPGLEAHHHISIPFPAVYVCIILNGMLTLIRHDSLHPMYFTLMLA 65  
QY 71 GDILSTSMRMLAIFWENSTTIOFDACLLQMFALHSGMESTVLLAMADRYAIC 130  
DB 66 GTDLMATLTTPVGMILWVNHREISSVGCFLDAVTFHSHSVESGSLMAYDRFAIR 125  
QY 131 HPLRAHATVLTLPRTKIGVAAVVGAAALMAPLPVFIKQLPFCNSNLSHSCYCLHODVMKL 190  
DB 126 NPLRAVSIITNRVIALAGVFLRGSVSLPVILRLFSFYSCKSHVITRAFCLOHEMLR 185  
QY 191 ACDDIRNVVYGLVITISAIGDSLISFSLILKLTGL-TREDAKAFGCVSHVCA 249  
DB 186 ACADIFENFLYVILSLITFLDLSLITLFSYIILMTVIGIASGEERAKALNTCISHISC 245  
QY 250 VLFETVYFGLSVNHRFSKRSDPLVILANTILVPPVNPVYGVKTEIKRIQLRL 308  
DB 246 VLFETVYFGLSVNHRFSKRSDPLVILANTILVPPVNPVYGVKTEIKRIQLRL 304  
  
RESULT 10  
OYB6\_HUMAN STANDARD; PRT; 313 AA.  
AC 096RD3;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Olfactory receptor 52E6.  
GN OR52E6.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE OF 70-287 FROM N.A.  
RA Fuchs T., Malceva B., Linhart C., Sharan R., Khen M., Herwig R.,  
RA Shmulevich D., Elkon R., Steinfath M., O'Brien J.K., Redelof U.,  
RA Lehrach H., Olender Z., Glusman G., Lancet D., Shamir R.;

RT DEPOG: a practical scheme for deciphering families of genes.\*;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC  
CC EMBL: AF399504; AAK94989.1; -  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm.1.1.  
DR PROSITE; PS00237; G\_PROTEIN\_RECP.F1.1; 1.  
DR PROSITE; PS00262; G\_PROTEIN\_RECP.F1.2; 1.  
DR G-protein coupled receptor; Transmembrane; glycoprotein;  
KW Multigene family; Olfaction.  
FT DOMAIN 1 27 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 28 51 1 (POTENTIAL).  
FT DOMAIN 52 59 2 (POTENTIAL).  
FT TRANSMEM 60 81 2 (POTENTIAL).  
FT DOMAIN 82 102 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 103 122 3 (POTENTIAL).  
FT DOMAIN 123 141 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 142 160 4 (POTENTIAL).  
FT DOMAIN 161 197 5 (POTENTIAL).  
FT TRANSMEM 198 220 6 (POTENTIAL).  
FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 238 260 7 (POTENTIAL).  
FT DOMAIN 261 295 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 276 295 7 (POTENTIAL).  
FT TRANSMEM 296 313 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 5 5 N-LINKED (GLCNAC. .) (POTENTIAL).  
SQ SEQUENCE 313 AA; 35523 MW; 6FC174BDDC20B83 CRC64;  
  
Query Match 43.6%; Score 708; DB 1; Length 313;  
Best Local Similarity 43.2%; Pred. No. 9,2e-47;  
Matches 140; Conservative 56; Mismatches 112; Indels 2; Gaps 2;  
  
QY 6 NNESSATYFLLGLPGLEAOFWLAFLPLCSLYLAIVAGNTTIIVTSHLEPNTFLCMS 70  
DB 5 NDTQFHTSFLGLIGLEVEVHNIGPFYSVILALSGAAIFVYQTQSLHEPNTYC 64  
QY 66 LCMISGIDILSTSMRMLAIFWENSTTIOFDACLLQMFALHSGMESTVLLAMADRF 125  
DB 65 LAMLDISLSTATIPKMLGIFWENIKESIFGYSOMFPIHFYVESIVVAAAFDR 124  
QY 126 YVAICHLRAHATVLTLPRTKIGVAAVVGAAALMAPLPVFIKQLPFCNSNLSHSCYCLHODVMKL 190  
DB 125 YVAICHLRAHATVLTLPRTKIGVAAVVGAAALMAPLPVFIKQLPFCNSNLSHSCYCLHODVMKL 184  
QY 186 DWKILACDDIRNVVYGLVITISAIGDSLISFSLILKLTGL-TREDAKAFGCVSHVCA 249  
DB 185 GIARLACASIKVIMFGL-GSISLLDVLITLISRIILXAVCLPSPWARKALATWCG 243  
QY 245 SHVCAVETFYFPGISLVNHRFSKRSDPLVILANTILVPPVNPVYGVKTEIKRIQLRL 308  
DB 244 SHIGVILAFSTPAFESFECFGHDIOYIHIFLANLYVVPPLNVIVGVKTRKIRRET 303  
QY 305 ILRLFAVATH 314  
DB 304 VLRIFFTDTH 313  
  
RESULT 11  
OXB4\_HUMAN STANDARD; PRT; 310 AA.  
ID OXB4\_HUMAN  
AC 09Y5P0;  
DT 16-OCT-2001 (Rel. 40, Created)

DN OR51B4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99238494; PubMed-10220430;  
 RA Bulger M., van Doornink J.H., Saitoh N., Telling A., Farrell C.M.,  
 RA Bender M.A., Felsenfeld G., Axel R., Groudine M.;  
 RT "Conservation of sequence and structure flanking the mouse and human  
 RT beta-globin loci: the beta-globin genes are embedded within an array  
 RT of odorant receptor genes.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:5129-5134(1999).  
 RN [2]  
 RP ERRATUM.  
 RA Bulger M., van Doornink J.H., Saitoh N., Telling A., Farrell C.M.,  
 RA Bender M.A., Felsenfeld G., Axel R., Groudine M.;  
 RL Proc. Natl. Acad. Sci. U.S.A. 96:8307-8307(1999).  
 RN [3]  
 RP REVISIONS.  
 RX MEDLINE-20570519; PubMed-11121057;  
 RA Bulger M., Bender M.A., van Doornink J.H., Wertman B., Farrell C.M.,  
 RA Felsenfeld G., Groudine M., Hardison R.;  
 RT "Comparative structural and functional analysis of the olfactory  
 RT receptor genes flanking the human and mouse beta-globin gene  
 RT clusters.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).  
 CC -1- FUNCTION: POTATIVE ODORANT RECEPTOR.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 -----  
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 -----  
 DR EMBL; AF137396; AAD29426.2; -  
 DR Genew; HGNC:14708; OR51B4.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR Pfam; PF00001; 7tm\_1; 1.  
 DR PRINTS; PR00237; GPCRHHODPSN.  
 DR PROSITE; PS00237; G-PROTEIN\_RECPT\_FL\_1; FALSE\_NEG.  
 DR PROSITE; PS50262; G-PROTEIN\_RECPT\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Olfaction.  
 FT DOMAIN 1 23  
 FT TRANSSEM 24 47  
 FT DOMAIN 48 55  
 FT TRANSSEM 56 77  
 FT DOMAIN 78 98  
 FT TRANSSEM 99 117  
 FT DOMAIN 118 136  
 FT TRANSSEM 137 155  
 FT DOMAIN 156 192  
 FT TRANSSEM 193 216  
 FT DOMAIN 217 233  
 FT TRANSSEM 234 256  
 FT DOMAIN 257 265  
 FT TRANSSEM 272 291  
 FT DOMAIN 292 310  
 FT DISULFID 95 186  
 FT CARBOHYD 4 4  
 SO SEQUENCE 310 AA; 34926 MM; BRE53363BA2RED67 CRC64;  
 Query Match 39.0%; Score 633; DB 1; Length 310;  
 Best Local Similarity 40.5%; Pred. NO. 4.2e-41;

Matches	122:	Conservative	72:	Mismatches	105:	Indels	2:	Gaps	2:
QY	10	SSATYFIIIGLPGLEAEAFWFLAFCLSCIXLLAVLGNLTITTYVTEHSLHEPMYIFLQML	69						
Db	5	NSAGGFLLTGFGEBAVHYRISMSEFFVYFSTIFEGNLTLLVLMNDHSLHEPMYFFLML	64						
QY	70	SGIDLLISTSSMKPLAIFWFMSTTIQPDACILQMFALHISLSCGMSYVLLAMAPRYVAI	129						
Db	65	ADTDLGMPFTFPPYVLVGLVLLDQREIADNACTQSF-IHSLAIYVSGLLVLAIDCFPAI	123						
QY	130	CHPLRHATVLTLPRTYKGVAAVVAAGALMLAPFRIKQLPFCRSENISSHSCYLDQDYMK	189						
Db	124	RTPRLAYNCLITNRSKRNINIGLVLMGFSILPILISLYCYPCGSRALLHFFCLADQVIK	183						
QY	190	LACDDIRVNVVYGLIIVTISAIGDLSLISFSYLLIKTVLGL-TREAQAKAFGTCVSHVC	248						
Db	184	LACADITFNHHIPIIQTSLTVEFDLILITFSYLLIKFTVMGIASQGEAKSLMTCVSHIS	243						
QY	249	AVETIYVYFGLSMWRHSKRSDSLPYVLIANYILVLPVLPNIYGVKTRIRRIIRL	308						
Db	244	CVLVEHITVMGLSTHRRGKHAPHVPPITMSYVHLFPPEVNPILITSIKTQIDQSIIRL	303						
QY	309	F 309							
Db	304	F 304							

RESULT 12

ID	Q2S2_HUMAN	STANDARD:	PRF:	319 AA.
AC	Q9N0N1			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Orfatory receptor 2S2.			
GN	OR2S2			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE OF 11-319 FROM N.A.			
RA	Cotby N.;			
RL	Submitted (APR-2000) to the EMBL/Genbank/DDBJ databases.			
CC	-1- FUNCTION: POTATIVE ODOANT RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	use by, non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or send an email to license@sib-sib.ch">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
DR	EMBL; AL135841; CAB96728.1; -			
DR	GeneW; HGNC:8276; OR2S2.			
DR	InterPro: IPR000276; GPCR_Rhodpsn.			
DR	Pfam; PF00001; 7tm_1; 1.			
DR	PRINTS; PR00237; GPCRHDOPSN.			
DR	PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.			
DR	PROSITE; PS0262; G_PROTEIN_RECPT_F1_2; 1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Multigene family; Olfaction.			
FT	DOMAIN	1	26	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	27	50	1 (POTENTIAL).
FT	DOMAIN	51	58	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	59	80	2 (POTENTIAL).
FT	DOMAIN	81	101	EXTRACELLULAR (POTENTIAL).
FT	TRANSSEM	102	121	3 (POTENTIAL).
FT	DOMAIN	122	140	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	141	159	4 (POTENTIAL).



FT DOMAIN 160 196 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 197 220 5 (POTENTIAL).  
 FT DOMAIN 221 237 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 238 260 6 (POTENTIAL).  
 FT DOMAIN 261 273 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 280 299 7 (POTENTIAL).  
 FT DOMAIN 300 319 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 98 190 BY SIMILARITY.  
 FT CARBOHYD 5 5 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 319 AA; 35172 MW; 602602RCA96A179F CRC64;

Query Match 28.8%; Score 468; DB 1; Length 319;  
 Best Local Similarity 35.6%; Pred. No. 1.3e-28;  
 Matches 114; Conservative 63; Mismatches 111; Indels 32; Gaps 9;

OY 8 NISSAAY-FILGL---PGLEAQFWLAPPCSLYLAVNLNTIYVTEHSHPM 63  
 DB 5 NETSPWGFVLLNSHAPLEKEFEVL---ILMTVLTLLGNVLLTITLDSRLHPM 61  
 OY 64 IFCLMISGIDILITSSMPKMLAFWFNSTTIOFDACLLQMFALHSLSGSEVTLAMAF 123  
 DB 62 FFLGNLSFDICTTSVPLVDLSFLPOTISFSACAVGMALSPMAAGTECLLSMAAF 121  
 OY 124 DRVACHELRATVTLRTKIGVAA-VKCAALMAPLVITKOLPFRSNTLSHC 182  
 DB 122 DRVACNPLRSVSKAYMFAASMAIGNASVHTSLAI-QLPFGDVIINHTFC 180  
 OY 183 LHODVAKLACDDIRVNVVGLIYIISAGLSLISFYLLIKTVGL-TREAQAFG 241  
 DB 181 ELIATVAKLACADISINVISKEVNTVFLGVPVLFISFSYFITTILRTSABEKRVFS 240  
 OY 242 TCVSVCAYFEIYVPEIGLSMVRHFSKRRDS-----PLFVILANTYLVPV 288  
 DB 241 TCSAHLTVIYFVGT---LEFMGKFKSKDSMGADKEDLSDKILPL-----FVGVTM 291  
 OY 289 LNPYGVGTEKRIORILRL 308  
 DB 292 LNPITLIRNKDKVKAARRL 311

RESULT 13  
 OL15\_MOUSE STANDARD; PRT; 312 AA.  
 ID OL15\_MOUSE  
 AC P23275;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Olfactory receptor 15 (OR3).  
 GN OLFR15.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93028384; PubMed=1384038;  
 RA Dione V.E., Hellemann S.F.;  
 RA "Spatial pattern of receptor expression in the olfactory epithelium";  
 RA Proc. Natl. Acad. Sci. U.S.A. 89:8948-8952(1992).  
 RL -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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DR EMBL; M84005; AAA39862.1; -  
 DR MGD; MGI:106182; Olfr15.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: pf00001; 7tm\_1; 1.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECPT\_FL1; 1.  
 DR PROSITE: PS50262; G\_PROTEIN\_RECPT\_FL2; 1.  
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KM Olfaction; Multigene family.  
 FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 25 48 1 (POTENTIAL).  
 FT DOMAIN 49 57 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 58 79 2 (POTENTIAL).  
 FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 101 120 3 (POTENTIAL).  
 FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 140 160 4 (POTENTIAL).  
 FT DOMAIN 161 200 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 201 222 5 (POTENTIAL).  
 FT TRANSMEM 223 236 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 237 261 6 (POTENTIAL).  
 FT DOMAIN 262 272 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 273 292 7 (POTENTIAL).  
 FT DOMAIN 293 312 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 97 189 BY SIMILARITY.  
 FT CARBOHYD 6 6 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 312 AA; 34333 MW; 8D387EBB51E132 CRC64;

Query Match 27.1%; Score 440; DB 1; Length 312;  
 Best Local Similarity 34.6%; Pred. No. 1.6e-26;  
 Matches 113; Conservative 65; Mismatches 123; Indels 26; Gaps 11;

OY 1 MNPVNGNSSATFILLGL---PGLEAQFWLAPPCSLYLAVNLNTIYVTEHS 57  
 DB 1 MEVDNSN---SSSGFILLMGSDHHELIFFAV---ILASYLLTIVGNLTITLSRLDAR 54  
 OY 58 LHEPMTIFCLMISGIDILITSSMPKMLAFWFNSTTIOFDACLLQMFALHSLSGSEV 117  
 DB 55 LHPMTIFELSLISLDAFTTSSVPMKMLMGPDKTSIGGCVTOLYVLMGATCCL 114  
 OY 118 LLAFAFRYVAICPLRHATVTLRTKIGVAAV-VKCAALMAPLVITKOLPFRCSN 175  
 DB 115 LVVAAPDRYVAVCRPLRTMYVAV-PRLC-WGIAAISGLSGSVISOSTTLOLPFGHR 172  
 OY 176 ILSHSYCLHODVAKLACDDIRVNVVGLIYIISAGLSLISFYLLIKTVGL-T 232  
 DB 173 KVDNFELEVPAMIRKLAGDGSILNEAVLNGVCTFTVPVAVIYV-SYCFIAGVAKIRS 230  
 OY 233 REAQAARFGTCVSHVCAVFIYVPEIGLSMVRHFSKRRDSPYILANTYLVPV 289  
 DB 231 VEGRRKAFNTCVSHLVVVFETG---SAIYGILPAKSSNOSGKFIISLYSVTPMV 285  
 OY 290 NPIYGVGTEKRIORILRLFHVATHAS 316  
 DB 286 NPLITLIRNKDKVKAARRLGKGRGAS 312

RESULT 14  
 OSFL\_HUMAN STANDARD; PRT; 314 AA.  
 ID OSFL\_HUMAN  
 AC G95221;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Olfactory receptor 5f1 (Olfactory receptor 11-10) (OR11-10).  
 GN OSFL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE OF 68-283 FROM N.A.  
 RX MEDLINE=99005533; PubMed=9787077;  
 RA Buettner J.A., Glusman G., Ben-Arie N., Ramos P., Lancet D.,

RA Evans G.A.:  
 RT "Organization and evolution of olfactory receptor genes on human  
 RL chromosome 11.";  
 RN Genomics 53:56-68(1998).  
 [12]  
 RP SEQUENCE OF 68-283 FROM N.A.  
 RA Fuchs T., Malecova B., Linhart C., Sharan R., Rhen M., Herwig R.,  
 RA Shmulevich D., Elkon R., Steinfach M., O'Brien J.K., Radcliff U.,  
 RA Lehnach H., Olander Z., Glusman G., Lancel D., Shamir R.,  
 RT "Derog: a practical scheme for deciphering families of genes.";  
 RL Submitted (Jul-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC  
 CC EMBL: AF065863; AAC70017.1; -  
 DR EMBL: AF399527; AAK95012.1; -  
 DR Genew: HGNC:8343; ORSFL.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PRINTS: PR00237; GPCR\_RHODOPSIN.  
 DR PROSITE: PS00237; G-PROTEIN\_RECP\_FL\_1; FALSE\_NEG.  
 DR PROSITE: PS50262; G-PROTEIN\_RECP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Olfaction.  
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 26 49 1 (POTENTIAL).  
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 58 79 2 (POTENTIAL).  
 FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 101 120 3 (POTENTIAL).  
 FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 140 158 4 (POTENTIAL).  
 FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 196 219 5 (POTENTIAL).  
 FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 237 259 6 (POTENTIAL).  
 FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 273 292 7 (POTENTIAL).  
 FT DOMAIN 293 314 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 97 189 BY SIMILARITY.  
 FT CARBOHYD 5 N-LINKED (GLCNAc... ) (POTENTIAL).  
 SO SEQUENCE 314 AA; 35131 MW; C14A9A35CD76E3A3 CRC64;  
 Query Match 26.8%; Score 435.5; DB 1; Length 314;  
 Best Local Similarity 32.7%; Pred. No. 3.6e-26;  
 Matches 102; Conservative 58; Mismatches 123; Indels 29; Gaps 6;  
 Oy 8 NESAATYFLIGLPLEAOFMLAPLCSLYLAIVAGNTLIYIVTRESLHEPMTFLC 67  
 Db 5 NTSLSFELVGLADPTLEQILFLPVIYTVLVGNLMLRLIDSOQLTPMPFLA 64  
 Oy 68 MLSGIDILSTSMKMLAIFENSTTIQFACLQNFALHISGNESTVLLAMAFDRV 127  
 Db 65 NLSFYDVCNSTIIPKMLADLSEKTIISFAGCELOMFISLATFECILQGLMAYDRA 124  
 Oy 128 AICHELRLAIVLTPRTKIGVAAYVGAALMAPLPEFIKOLPECRNLSLSYCLHODV 187  
 Db 125 AICRPLILSLMSFTVYKMAAGAFAGLNFMTVNTSVHSLSISFDSNVIIHFCDSPPL 184  
 Oy 188 MTLACDD-----IRVVVYGLVYIISAGIDSLISFVLLIKTVLGL-TREA 235  
 Db 185 FTLSCSDVTLLESISIIAGNAVIGTLVLLS-----SYSLVLP--SIFSMSGE 233  
 Oy 236 QAKAGCTCVSHVCAVFIYVP--FIGLSMVRHSKRSDPLVLIANILVLPVLANIV 293

Db 234 KRAEFTSCASHLTAITLFTATCTIYLRPSSSYLNDK-----VASFTVTVLPMNLPI 289.  
 Oy 294 YGVTKREIRORI 305  
 Db 290 YSLRSKEVKAL 301  
 RESULT 15  
 ID OLFL4\_RAT STANDARD; PRT; 312 AA.  
 AC P23273;  
 DT 01-NOV-1991 (rel. 20, Created)  
 DT 01-NOV-1991 (rel. 20, Last sequence update)  
 DE Olfactory receptor-like protein 114.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-91191556; PubMed-1840504;  
 RA Buck L., Axel R.;  
 RT "A novel multigene family may encode odorant receptors: a molecular  
 RT basis for odor recognition.";  
 RL Cell 65:175-187(1991).  
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC  
 CC EMBL: M64391; AAA41754.1; -  
 DR PIR: I23701; I23701.  
 DR InterPro: IPR000276; GPCR\_Rhodopsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PROSITE: PS00237; G-PROTEIN\_RECP\_FL\_1; 1.  
 DR PROSITE: PS50262; G-PROTEIN\_RECP\_FL\_2; 1.  
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;  
 KW Multigene family; Olfaction.  
 FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 26 49 1 (POTENTIAL).  
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 58 79 2 (POTENTIAL).  
 FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 101 120 3 (POTENTIAL).  
 FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 140 158 4 (POTENTIAL).  
 FT DOMAIN 159 196 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 197 219 5 (POTENTIAL).  
 FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 237 260 6 (POTENTIAL).  
 FT DOMAIN 261 272 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 273 292 7 (POTENTIAL).  
 FT DOMAIN 293 312 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 97 189 N-LINKED (GLCNAc... ) (POTENTIAL).  
 FT CARBOHYD 5 BY SIMILARITY.  
 SO SEQUENCE 312 AA; 35718 MW; 08F68546994B1680 CRC64;  
 Query Match 26.8%; Score 434.5; DB 1; Length 312;  
 Best Local Similarity 33.5%; Pred. No. 4.2e-26;  
 Matches 105; Conservative 64; Mismatches 119; Indels 25; Gaps 7;  
 Oy 8 NESAATYFLIGLPLEAOFMLAPLCSLYLAIVAGNTLIYIVTRESLHEPMTFLC 67  
 Db 105 NTSLSFELVGLADPTLEQILFLPVIYTVLVGNLMLRLIDSOQLTPMPFLA 64



```

Db      5  NOTLLEFLGLPIPEYHLLFYALFLAMYLITIIIGNLLIIVRLDSHLMPYLFIS 64
QY      68  MLSGIDILISTSPMKMLAIFWPNSTTIOFDACILOMFAHSLSGNESTVILAMAFDRYV 127
Db      65  NLSFSDLCPSSVTMPKLLQNNQSOVPSISYTGCLTQLTFEYFEGDMSPLLVMAVDRTV 124
QY      128  AICHPLRHATVTLTPRVTKIGVAANV-----RGAALMAPLPVEFIKOLPECRSNILSHSY 181
Db      125  AICPPLARTTINS---TRFCASLVLLMMLMTFHALHTL--LIARLSFCEKNVILHFF 178
QY      182  CLHODVMTLACDDIRVN-----VYGLVIISAGLSLISFSTYLLIKTVLGL-TREA 235
Db      179  CDISALMLKLSGSDIYNELMAYIILGGLIITII-----PFLIYMSYVRIFFSILKFPISIOD 233
QY      236  QAKAFGTCVSHCAVEFIYVPEIGLSWVHRSKRSDPLPVILANIYLLVPVLPYVYG 295
Db      234  IYVSTGSHLSVYTLFGIIFGIYICP---SGNNTYKEIMAMKTYVVTPLNPFYIS 291
QY      296  VTKETIRQRIQL 308
Db      292  LNRDMKRRLIRV 304

```

Search completed: March 26, 2003, 09:53:02  
 Job time : 26 secs

GenCore version 5.1.4.P5.4578  
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OM protein - protein search, using sw model

Run on: March 26, 2003, 09:51:52 ; Search time 87 Seconds

(without alignments)  
753.138 Million cell updates/sec

Title: US-09-966-459A-2

1623

Sequence: 1 MWDPNNGESSATYFILIGL.....KEIRORILRLFHVATHASEP 318

Scoring table:

BLOSUM62

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL\_21:\*  
2: sp\_archaea:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1618	99.7	317	4	08TCB6
2	1516	93.4	317	11	08VG27
3	989	60.9	320	11	08VBV9
4	971.5	59.9	322	11	08VFO9
5	918.5	56.6	315	11	08VHO5
6	901.5	55.5	312	11	08VH11
7	879.5	54.2	314	11	08VG26
8	877.5	54.1	318	11	08VG23
9	877	54.0	313	11	08VH17
10	871.5	53.7	314	11	08VG22
11	866.5	53.4	317	11	08VH01
12	861.5	53.1	319	11	08VG28
13	858	52.9	317	11	08VH04
14	857.5	52.8	319	11	08VGW0
15	856.5	52.8	319	11	09EQ07
16	856	52.7	317	11	08VEX9

17	844.5	52.0	319	11	08VG99	08VG99 mus musculus
18	842.5	51.9	312	11	08VGX6	08VGX6 mus musculus
19	839.5	51.7	314	11	08VH15	08VH15 mus musculus
20	839	51.7	330	11	08VFO7	08VFO7 mus musculus
21	838	51.6	316	11	08VG78	08VG78 mus musculus
22	837.5	51.6	317	11	08VGX8	08VGX8 mus musculus
23	835.5	51.5	317	11	08VGX8	08VGX8 mus musculus
24	832	51.3	312	11	08VH12	08VH12 mus musculus
25	831.5	51.2	314	11	08VG85	08VG85 mus musculus
26	831.5	51.2	319	11	08VG76	08VG76 mus musculus
27	830	51.1	316	11	08VG79	08VG79 mus musculus
28	830	51.1	318	11	08VH16	08VH16 mus musculus
29	828.5	51.0	327	11	08VFE8	08VFE8 mus musculus
30	827.5	51.0	329	11	08VGX9	08VGX9 mus musculus
31	826.5	50.9	316	11	08VG20	08VG20 mus musculus
32	825.5	50.9	315	11	08VG75	08VG75 mus musculus
33	822.5	50.7	312	11	08VFO2	08VFO2 mus musculus
34	820	50.5	319	13	09YH55	09YH55 gallus gall
35	818	50.4	315	11	08VG23	08VG23 mus musculus
36	815.5	50.2	314	11	08VH21	08VH21 mus musculus
37	814.5	50.2	313	11	08VG74	08VG74 mus musculus
38	810	49.9	312	11	08VGW2	08VGW2 mus musculus
39	807.5	49.8	321	11	08VH20	08VH20 mus musculus
40	807	49.7	326	11	09VWD9	09VWD9 mus musculus
41	806	49.7	323	11	08VG75	08VG75 mus musculus
42	805.5	49.6	321	11	08VH19	08VH19 mus musculus
43	800	49.3	316	11	09EQ05	09EQ05 mus musculus
44	800	49.3	317	11	08VH13	08VH13 mus musculus
45	798	49.2	318	11	08VH14	08VH14 mus musculus

## ALIGNMENTS

RESULT 1  
ID 08TCB6 PRELIMINARY: PRT; 317 AA.  
AC 08TCB6  
DT 01-JUN-2002 (TRENBERG, 21, Created)  
DT 01-JUN-2002 (TRENBERG, 21, Last sequence update)  
DT 01-JUN-2002 (TRENBERG, 21, Last annotation update)  
DE Hypothetical 35.3 kDa protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LUNG;  
RA Strusberg R.;  
RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC022401; AAH22401.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 317 AA; 35271 MW; 8C7293AA7BCA95C CRC64;

Query Match 99.7%; Score 1618; DB 4; Length 317;

Best Local Similarity 100.0%; Pred. No. 1.6e-137; Indels 0; Gaps 0;  
Matches: 317; Conservative 0; Mismatches 0;

QY	2	MWDPNNGESSATYFILIGLPGLEEAQFWLAFPLCSYLLAVLGNLTIIYIVREHSIHP	61
DB	1	MWDPNNGESSATYFILIGLPGLEEAQFWLAFPLCSYLLAVLGNLTIIYIVREHSIHP	60
QY	62	MYFLCMLSGIDILISTSSPKKLAIFWENSTTIQDACLQWFAIHSLSGMSYVLAM	121
DB	61	MYFLCMLSGIDILISTSSPKKLAIFWENSTTIQDACLQWFAIHSLSGMSYVLAM	120
QY	122	APFRVYAIHPHARVLTLPRTKIGVAAVVGALMLPVEITQLPCCRNIISHSY	181
DB	121	APFRVYAIHPHARVLTLPRTKIGVAAVVGALMLPVEITQLPCCRNIISHSY	180
QY	182	CLHQDVKLACDDIRNVVYGLVIVISAIGLDSLLISFYLLIKTVLGLFRQAQAKG	241
DB		CLHQDVKLACDDIRNVVYGLVIVISAIGLDSLLISFYLLIKTVLGLFRQAQAKG	241

Db 181 CLHODVAKLACDDIRVNVYGLIIVISAIGDSLISFYLILKTVGLGPREDAKAFG 240  
 QY 242 TCVSVCVAVFIFYFPIGSLSVHRFSKRSDPLPVILANITLVPVLPVPIYGVKTKREI 301  
 Db 241 TCVSVCVAVFIFYFPIGSLSVHRFSKRSDPLPVILANITLVPVLPVPIYGVKTKREI 300  
 QY 302 RQRLRLFHVATHASEP 318  
 Db 301 RQRLRLFHVATHASEP 317

## RESULT 2

Q8V6Z7 PRELIMINARY; PRT; 317 AA.  
 AC Q8V6Z7;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Olfactory receptor MOR18-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang X., Firestein S.J.;  
 RT "The olfactory receptor gene superfamily of the mouse."  
 RL Nat. Neurosci. 0:0-0(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AY072993; AAL60656.1; -;  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECCEP\_FL1; UNKNOWN\_1.  
 DR PROSITE: PS0262; G\_PROTEIN\_RECCEP\_FL2; 1.  
 KM Receptor.  
 SQ SEQUENCE 317 AA; 35463 MW; 5A0E59E229852534 CRC64;

Query Match 93.4%; Score 1516; DB 11; Length 317;  
 Best Local Similarity 93.7%; Pred. No. 2,3e-128;  
 Matches 296; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 2 MWDNGNESSATYFLLGLPELEAQTFLAPPLCSLYILAVLGNLTIIYVTRHSHLHP 61  
 Db 1 MWDNGNESSATYFLLGLPELEAQTFLAPPLCSLYILAVLGNLTIIYVTRHSHLHP 60  
 QY 62 MYIFGLMSGDIILISTSMKMLATFMENTTIOFDACLQMFRAHISLSGMESTVLLAM 121  
 Db 61 MYIFGLMSGDIILISTSMKMLATFMENTTIOFDACLQMFRAHISLSGMESTVLLAM 120  
 QY 122 AFDRYVAICHLRAATVLTLPRTYKIGVAAVVGAAALMAPLPVFILKQDPCFRSNILSHY 181  
 Db 121 AFDRYVAICHLRAATVLTLPRTYKIGVAAVVGAAALMAPLPVFILKQDPCFRSNILSHY 180  
 QY 182 CLHODVAKLACDDIRVNVYGLIIVISAIGDSLISFYLILKTVGLGPREDAKAFG 241  
 Db 181 CLHODVAKLACDDIRVNVYGLIIVISAIGDSLISFYLILKTVGLGPREDAKAFG 240  
 QY 242 TCVSVCVAVFIFYFPIGSLSVHRFSKRSDPLPVILANITLVPVLPVPIYGVKTKREI 301  
 Db 241 TCVSVCVAVFIFYFPIGSLSVHRFSKRSDPLPVILANITLVPVLPVPIYGVKTKREI 300  
 QY 302 RQRLRLFHVATHASEP 317  
 Db 301 RQRLRLFHVATHASEP 316

RESULT 3  
 Q8V6V9 PRELIMINARY; PRT; 320 AA.  
 ID Q8V6V9;  
 AC Q8V6V9;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Olfactory receptor MOR18-2 (Prostate-specific G protein-coupled receptor RALG).  
 GN OLF78.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Zhang X., Firestein S.J.;  
 RT "The olfactory receptor gene superfamily of the mouse."  
 RL Nat. Neurosci. 0:0-0(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Adams M.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA STRAIN-BALB/C;  
 RX MEDLINE-21564169; PubMed-11707321;  
 RA Yuan T.T., Toy P., McClary J.A., Lin R.J., Miyamoto N.G.,  
 RA Kretschmer P.J.;  
 RT "Cloning and genetic characterization of an evolutionarily conserved  
 human olfactory receptor that is differentially expressed across  
 species."  
 RL Gene 278:41-51(2001).  
 DR EMBL: AY073011; AAL60674.1; -;  
 DR EMBL: AF378854; AAL35109.1; -;  
 DR MGI: 2157548; Olf78.  
 DR InterPro: IPR000276; GPCR\_Rhodpsn.  
 DR Pfam: PF00001; 7tm\_1; 1.  
 DR PROSITE: PS00237; G\_PROTEIN\_RECCEP\_FL1; UNKNOWN\_1.  
 DR PROSITE: PS0262; G\_PROTEIN\_RECCEP\_FL2; 1.  
 KM Receptor.  
 SQ SEQUENCE 320 AA; 35577 MW; 7161ACABF4328959 CRC64;

Query Match 60.9%; Score 989; DB 11; Length 320;  
 Best Local Similarity 60.1%; Pred. No. 5,3e-81;  
 Matches 184; Conservative 52; Mismatches 68; Indels 2; Gaps 2;

QY 8 NESSATYFLLGLPELEAQTFLAPPLCSLYILAVLGNLTIIYVTRHSHLHPYIFLC 67  
 Db 5 NESSATYFLLGLPELEAQTFLAPPLCSLYILAVLGNLTIIYVTRHSHLHPYIFLC 63  
 QY 68 MLCGDIILISTSMKMLATFMENTTIOFDACLQMFRAHISLSGMESTVLLAMFDRYV 127  
 Db 64 MLCGDIILISTSMKMLATFMENTTIOFDACLQMFRAHISLSGMESTVLLAMFDRYV 123  
 QY 128 AICHLRAATVLTLPRTYKIGVAAVVGAAALMAPLPVFILKQDPCFRSNILSHYCLHODV 187  
 Db 124 AICHLRAATVLTLPRTYKIGVAAVVGAAALMAPLPVFILKQDPCFRSNILSHYCLHODV 183  
 QY 188 MLCACDDIRVNVYGLIIVISAIGDSLISFYLILKTVGLGPREDAKAFGTVSH 246  
 Db 184 MLCACDDIRVNVYGLIIVISAIGDSLISFYLILKTVGLGPREDAKAFGTVSH 243  
 QY 247 VCAVFIFVPIGSLSVHRFSKRSDPLPVILANITLVPVLPVPIYGVKTKREI 306  
 Db 244 VCAVFIFVPIGSLSVHRFSKRSDPLPVILANITLVPVLPVPIYGVKTKREI 303  
 QY 307 RLFAVA 312  
 Db 304 AMFKIS 309

RESULT 4  
 Q8VFO9 PRELIMINARY; PRT; 322 AA.  
 ID Q8VFO9;  
 AC Q8VFO9;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)

```

DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Olfactory receptor MOR18-3.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RL EMBL: A1072932; AL61395.1;
DR InterPro: IPR002106; AATRNA_1ligaseII.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PROSITE: PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEPTOR_FL_2; 1.
KW Receptor.
SQ SEQUENCE 322 AA; 35612 MW; D40302782D4B2FEF6 CRC64;

Query Match 59.9%; Score 971.5; DB 11; Length 322;
Best Local Similarity 58.5%; Pred. No. 2e-79;
Matches 182; Conservative 58; Mismatches 68; Indels 3; Gaps 3;

OY 1 MANDPNGNSSATYFTLIGLPGLE-EEAOFWIAAPLCLYLAVGNLTIIYVTEHSLH 59
DB 8 LIATPGSLAHPRFLLVIGLPGSKIHFLAPLPCFMVAVATLGNALIFITRVERRLH 67
OY 60 EPRATLCMSGIDILISTSSMRKMAIFNFNSTTIOFDACLLQNEAHSLSGHESTVLL 119
DB 68 EPRATLCMSGIDILISTSSMRKMAIFNFNSTTIOFDACLLQNEAHSLSGHESTVLL 127
OY 120 AMAFDRVAICHPLEHATVTLPRVTRIGVAAYVGAALAPLPVFVKOLPFCRSNTLSH 179
DB 128 AMAFDRVAICHPLEHATVTLPRVTRIGVAAYVGAALAPLPVFVKOLPFCRSNTLSH 187
OY 180 SYCLHODVAKLACDIRVNVVGLIVTISAIGLSDLSISFYLLIKTVLGL-TREAQAK 238
DB 188 SYCLHODVAKLACDIRVNVVGLIVTISAIGLSDLSISFYLLIKTVLGL-TREAQAK 247
OY 239 ABECTSHVCAVFIYVPGFGLSMNRHRSKRSDPLVYLIANTYLLVPLNPIYGVKT 298
DB 248 ABECTSHVCAVFIYVPGFGLSMNRHRSKRSDPLVYLIANTYLLVPLNPIYGVKT 306
OY 299 KEIRRIARLE 309
DB 307 KEIRRIARLE 317

RESULT 5
OYVH05 PRELIMINARY; PRT; 315 AA.
AC OYVH05;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Olfactory receptor MOR10-1.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]

```

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RP SEQUENCE FROM N.A.
RA Adams M.;
RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RL EMBL: A1072983; AL60646.1;
DR InterPro: IPR002106; AATRNA_1ligaseII.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PROSITE: PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEPTOR_FL_2; 1.
KW Receptor.
SQ SEQUENCE 315 AA; 35157 MW; BAA50EF966E3F0A9 CRC64;

Query Match 56.6%; Score 918.5; DB 11; Length 315;
Best Local Similarity 54.9%; Pred. No. 1.1e-74;
Matches 169; Conservative 64; Mismatches 74; Indels 1; Gaps 1;

OY 3 VDPNGNSSATYFTLIGLPGLE-EEAOFWIAAPLCLYLAVGNLTIIYVTEHSLH 62
DB 1 MNSASQTNHSHFLLTGIPGMPDKNPMWAFGLFTYLLTLLNGCTLLAVKVEQSLHEPM 60
OY 63 YIFLCMSGIDILISTSSMRKMAIFNFNSTTIOFDACLLQNEAHSLSGHESTVLLAMA 122
DB 61 YIFLCIALTDVSLSMSTPSMLSTFENFNAPEIPDCACTOMFPIHGGVSGVLSMA 120
OY 123 FDRVAICHPLEHATVTLPRVTRIGVAAYVGAALAPLPVFVKOLPFCRSNTLSH 182
DB 121 FDRVAICHPLEHATVTLPRVTRIGVAAYVGAALAPLPVFVKOLPFCRSNTLSH 180
OY 183 LHODVAKLACDIRVNVVGLIVTISAIGLSDLSISFYLLIKTVLGL-TREAQAKFG 241
DB 181 LHODVAKLACDIRVNVVGLIVTISAIGLSDLSISFYLLIKTVLGL-TREAQAKFG 240
OY 242 TCYSHVCAVFIYVPGFGLSMNRHRSKRSDPLVYLIANTYLLVPLNPIYGVKTKEI 301
DB 241 TCYSHVCAVFIYVPGFGLSMNRHRSKRSDPLVYLIANTYLLVPLNPIYGVKTKEI 300
OY 302 RRIARLE 309
DB 301 RRIARLE 308

RESULT 6
OYVH11 PRELIMINARY; PRT; 312 AA.
AC OYVH11;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE Olfactory receptor MOR7-2.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
RL EMBL: A1072977; AL60640.1;
DR InterPro: IPR002106; AATRNA_1ligaseII.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PROSITE: PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEPTOR_FL_2; 1.
KW Receptor.
SQ SEQUENCE 312 AA; 34574 MW; CD233B37732052E5 CRC64;

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	Query Match	55.5%	Score 901.5;	DB 11;	Length 312;	
	Best Local Similarity	53.2%	Pred. No. 3.8e-73;			
	Matches 165; Conservative	63;	Mismatches 81;	Indels 1;	Gaps 1;	
OY	1 MAMDPNGNESSATYFYLIGLPGLEBAQFWLAFLCSLYLVANGLMITYIVRTSHSLHE 60					
Db	1 MTPGPIYGKSSMSSTFLLSGIPGLEHMHIMISLPCLAMTVLSITLGCTLIETIKTEPSLHE 60					
OY	61 PMYIYLCMLSGIDILISTSSMPKMAITWFNSTTIQFDACLOMFALHSLSGESTVTLIA 120					
Db	61 PMYELSMIALTDICLSICTLETPTVLGIWFGARDISHACFEOLFPHICLSFTLESVYLS 120					
OY	121 MAFDENVAIICHPLRBATVLLPRTVKIGVAAYVRGAALMAPVPVRIKOLPCRSNIIISH 180					
Db	121 MAEDFVAICRPLHASTLTHTVIIRIGIASGRSVALFPPEMKRPVCGSLVLSHS 180					
OY	181 YCIHADVMKLCCDDIRNVVVYGLIYISAGIDSLISESYLLIETKVGLT-TREAQAKA 239					
Db	181 YCLOBEYVKMLCADIKANSIYGMFIYVSQVDILLILESYLLIRTYLSTASRAERLKA 240					
OY	240 FGTGVSHVCAMFIFVTYPGLISMVHRFSKRDSPLPVILIANTYLLVPVLANDIYGVKTK 299					
Db	241 INTFCVSHISAVALFYTPMIGLSVIRHFGRQAPHLVQVVGFFYLLPPVAMPNDIYSVKTK 300					
OY	300 ETRORILRLP 309					
Db	301 QIRDRVAAAF 310					
	RESULT 7					
ID	08VGZ6 PRELIMINARY; PRF; 314 AA.					
AC	08VGZ6;					
DT	01-MAR-2002 (TREMBLrel. 20, Created)					
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)					
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)					
DE	Olfactory receptor MOR14-2.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.					
OX	NCB1_Taxid-10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Zhang X., Firestein S.J.;					
RT	"The olfactory receptor gene superfamily of the mouse."					
RL	Nat. Neurosci. 0:0-0(2002).					
RN	[2]					
RE	SEQUENCE FROM N.A.					
RA	Adams M.;					
RL	Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.					
DR	EMBL; AY072994; AAL60657.1;					
DR	InterPro; IPR002106; AATRN_LigaseII.					
DR	InterPro; IPR000276; GPCR_Rhodopsn.					
DR	Pfam; PF00001; Tm_1.1.					
DR	PROSITE; PS00339; AA_TRNA_LIGASE_I1_2; UNKNOWN_1.					
DR	PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.					
DR	PROSITE; PS50262; G_PROTEIN_RECP_F1_2; 1.					
KW	Receptor.					
SQ	SEQUENCE 314 AA; 35096 MW; 9F1016F8B1A040E9 CRC64;					
	Query Match 54.2%; Score 879.5; DB 11; Length 314;					
	Best Local Similarity 52.6%; Pred. No. 3.6e-71;					
	Matches 163; Conservative 62; Mismatches 82; Indels 3; Gaps 2;					
OY	5 PNGNSSA--TFYILIGLGEAEQFMALFPLCSLYLVANGLNTIIVRTSHSLHEPN 62					
Db	2 PSFNSTAIAPPYFLLTGIPGLTSTHWTSIPCCCLAINAISNSMLFPIITISSLHEPN 61					
OY	63 YIFLCMLSGIDILISTSSMPKMAITWFNSTTIQFDACLOMFALHSLSGESTVTLIA 122					
Db	62 YIFLSMLSTDTGCLSLTVYVIGLFMWVREIRSPACIGQMFFIHGFPMSSVYLVYA 121					
OY	123 EDRIYAICHPLRHATVLLPRTVKIGVAAYVRGAALMAPVPVRIKOLPCRSNIIISHSYC 182					

Dd	122	FDRFALICNPILRYAMILLNSRIANGFAIIIRGTALTALVPLLLKRLSPGCSHVLHHSYC	181
Oy	183	LHQDWAKIACDDIRAVNVYGLIVITISAIGDLSLISFSTLLIKTVLGL-TREAOAKAF	241
Dd	182	FHPDMKLSCSPTSRINSAGLAIVISTAGIDSVLLISLVLIHSHVLCIASKEEKKAFG	241
Oy	242	TGVSHVCVAFIFYYVFIGLSMWHRSKRDSPLVIILANIYLVPVLPNIYGYKTEI	301
Dd	242	TCVSHLSVALEFYIPMISLTLVHRGKNAPEPVHTLIANVYLLIPPVMNPIIYSVKTKOI	301
Oy	302	RORILRFHV 311   : :   :	
Dd	302	KRAMLFVEFV 311	
RESULT 8			
OBYGZ3 PRELIMINARY: PRT: 318 AA.			
Ac	OBYGZ3		
Dt	01-MAR-2002 (TREMBLrel. 20. Created)		
Dt	01-MAR-2002 (TREMBLrel. 20. Last sequence update)		
Dt	01-JUN-2002 (TREMBLrel. 21. Last annotation update)		
De	Olfactory receptor MOR10-2.		
Os	Mus musculus (Mouse).		
Oc	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Ox	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
Rn	NCBI_Taxid=10090;		
Rn	[1]		
Rp	SEQUENCE FROM N.A.		
Ra	Zhang X., Firestein S.J.;		
Rt	"The olfactory receptor gene superfamily of the mouse."		
Rl	Nat. Neurosci. 0:0-0(2002).		
Rn	[2]		
Rp	SEQUENCE FROM N.A.		
Ra	Adams M.;		
Rl	Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.		
Dt	EMBL; AY072997; AAL0660.1; -		
Dt	InterPro: IPR002106; AATRNA_1lgaseII.		
Dt	InterPro: IPR001064; Crystallin.		
Dt	InterPro: IPR000276; GPCR_Rhodopsn.		
Dt	Pfam: PF00001; Tm1.1; 1.		
Dr	PROSITE; PS00339; AA_TRNA_LIGASE_IL2; UNKNOWN_1.		
Dr	PROSITE; PS00225; CRYSTALLIN_BETA_GAMMA; UNKNOWN_1.		
Kr	PROSITE; PS50262; G_PROTEIN_REC_P1_2; 1.		
Kr	Receptor.		
Sq	SEQUENCE 318 AA; 35593 MW; 3A6969E821087E48 CRC64;		
Query Match	54.1%; Score 877.5; DB 11; Length 318;		
Best Local Similarity	54.7%; Pred. No. 5.6e-71;		
Matches 169; Conservativity	54; Mismatches 85; Indels 1; Gaps 1;		
Oy	2 HYDPGNSSAYEFLLIGPGLGEQFWLAPLGSGIYLAIVNGNTLIYIVTRESLSEP	61	
Dd	1 MADHHSSQSCHLITLTGPGLEOKTYMAAPFLGAITYALAENGVSIIITSSESLHIP	60	
Oy	62 MYIFCLMSGDILITSSTSMPEPMALIFWENSTTIQFDACLQMFIAHLSLGMESTVLLAM	121	
Dd	61 MYIFCLMALADMGILTCTPLSMGLGFEMFNKYFTFDCGLVQMYFIHFSAIESGLVAM	120	
Oy	122 AFDRYAVALCHPRLKRAVTULTPVRNYIGAVALAAVYRGALAAPLDFVFKOLPFRCNSILISHY	181	
Dd	121 AIDRYIALVSWPLRSTGITLLNGVCKIGMLISRACVYPVPFLTKRLRPFRSNLSISF	180	
Oy	182 CLHQOVMLACODDIRVNVYGLIVISAIGDLSLISFSYLLIKTVLGL-TREAQAKAF	240	
Dd	181 CLHQOVMLACASTVNSLIGLAIVTFKGSDSLISLYFILTLMVAINSGEBRLAKL	240	
Oy	241 GTCVSHVCVAFIFYYVFIGLSMWHRSKRDSPLVIILANIYLVPVLPNIYGYKTEI	300	
Dd	241 NTGVSHICAVLIFYPYDLIGVSIVIHRRGKHLSPLTALMANNAVLPVLPNIYGYKTEI	300	
Oy	301 IKORILRLF 309		

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Db 301 IRRKIIOIF 309

RESULT 9
ID 08VH17 PRELIMINARY; PRT; 313 AA.
AC 08VH17;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Olfactory receptor MOR1-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AY072971; AAL60634.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KM Receptor.
SQ SEQUENCE 313 AA; 35682 MW; 39476E03FD201D6C CRC64;

Query Match 54.08; Score 877; DB 11; Length 313;
Best Local Similarity 51.88; Pred. No. 6.1e-71;
Matches 158; Conservative 72; Mismatches 73; Indels 2; Gaps 2;

OY 6 NGNSSATYFLLIGLPGLAEQFMAFLPCLSLYLIANGLNTIYIVREHSLHEPYIF 65
Db 6 NSLSQKATFF LTFQGLEHREHGISIPFCSTIYLIYILNLTIAVTRDTALHEPITYF 64
OY 66 LCMISGIDILISTSSMRKLAIFWENSTTIQFDACLQMPAHSLSGMESTVLLAMADR 125
Db 65 LAMLAADLGLCLSTLPVIGIFWDAEIGIPACFTQLFHTLSLVESVLLMSRDR 124
OY 126 YVAICHPRLRAATVLTLPRTKIGVAAVGAALMAPLPVFIKQLPFCRSNLTSLCHQ 185
Db 125 YVAICNPLRSTIITPRRIYKMGISVLRSAALLPLPFLIKRHRYSVLAHAYCIHL 184
OY 186 DVMKLADDIRVNVVGLIYISAIGLSLISFYLILKTVLG-LTREQAARFGTCV 244
Db 185 EIMKLACSSIIYVNIYGLFVYACTGVDSLITFLSTYLLIAHAYGKASROERLALNCCI 244
OY 245 SHVCAVFLYVPFGLSNVHRESKRSDPLPVILANIYLLVPPVILVGVKTKELROR 304
Db 245 SHICAVLFLYPMGLSLVHRGSEHLPRIYHLLMSYTYLLVPLNPIVYSIKTKOIROR 304
OY 305 ILRLP 309
Db 305 IIRKE 309

RESULT 10
ID 08VGZ2 PRELIMINARY; PRT; 314 AA.
AC 08VGZ2;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Olfactory receptor MOR30-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AY072998; AAL60661.1;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KM Receptor.
SQ SEQUENCE 314 AA; 35577 MW; 71BEEF2F351F669 CRC64;

Query Match 53.78; Score 871.5; DB 11; Length 314;
Best Local Similarity 50.28; Pred. No. 1.9e-70;
Matches 153; Conservative 68; Mismatches 85; Indels 1; Gaps 1;

OY 2 MWDPNGSSATYFLLIGLPGLAEQFMAFLPCLSLYLIANGLNTIYIVREHSLHEP 61
Db 1 MWASSNSSHPLFPMALGIPGLYENQWIAFPFCVMTYVALTGNTIYIRIDHTLHEP 60
OY 62 MYTLCMISGIDILISTSSMRKLAIFWENSTTIQFDACLQMPAHSLSGMESTVLLAM 121
Db 61 MYTFLALATDLVLSSTQPKMALIIFSHSETEYNACLIQVFIHAFSSVESGVLTMT 120
OY 122 AFDRYVAICHPRLRAATVLTLPRTKIGVAAVGAALMAPLPVFIKQLPFCRSNLTSLSHY 181
Db 121 ALDRYVAICHPRLRSSTITTSVTKGAAVVRLGLMWSPECFVSNMPPNVIYIQSY 180
OY 182 CLHODVAKLADDIRVNVVGLIYIISAIGLSLISFYLILKTVLG-LTREQAARF 240
Db 181 CEHNAVLYKLYCADRVNKGIGLFAFVGVGDIIVISYVMILRAVLRPSGARAKAF 240
OY 241 GTCVSHVCAVFLYVPFGLSNVHRESKRSDPLPVILANIYLLVPPVILVGVKTE 300
Db 241 GTCASHVCVLIATFYLPALFTFLTRFGHVPVRAVHINAFNYLPALNPIITGVTRKO 300
OY 301 IRRKIIRLF 309
Db 301 IRRVIRGF 309

RESULT 11
ID 08VH01 PRELIMINARY; PRT; 317 AA.
AC 08VH01;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Olfactory receptor MOR19-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 0:0-0(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Adams M.;
RT Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AY072967; AAL60650.1;
DR InterPro: IPR002106; ATRNA_11gaseit.
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.

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ID	ORGANO	PRELIMINARY;	PRT;	319 AA.
AC	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DE	Olfactory receptor MOR30-2.			
OS	Mus musculus (Mouse).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RA	SEQUENCE FROM N.A.			
RP	Zhang X., Firestein S.J.;			
RT	"The olfactory receptor gene superfamily of the mouse.";			
RL	Nat. Neurosci. 0:0-0(2002).			
RM	[2]			
RP	SEQUENCE FROM N.A.			
RA	Adams M.;			
RL	Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AY073034; AL60697.1;			
DR	InterPro: IPR000276; GPCR_Rhodopsn.			
DR	Pfam: PF00001; 7tm1.1; 1			
DR	PROSITE: PS00237; G_PROTEIN_RECIP_F1.1; UNKNOWN_1.			
DR	PROSITE: PS50262; G_PROTEIN_RECIP_F1.2; 1.			
RM	Receptor.			
SO	SEQUENCE 319 AA; 35988 MW; B2DBA1465A063F CRC64;			
Query Match	52.8%; Score 857.5; DB 11; Length 319;			
Best Local Similarity	49.48; Pred. No. 3.5e-69;			
Matches 154; Conservative	67; Mismatches 90; Indels 1; Gaps 1			
OY	1 MMYDNGNESSATFILLGLPGLEEAQFMLAPLCSLYIAVIGNTLIIYVTEHSLH 60			
DB	5 LMLASRNSSSHETFFILGIPLENQGFVAPFPFCMTIVATGNTILAIIRIDITLH 64			
OY	61 PWTIFLMLSGIDILISTSSMPKMAIFENSTTIOFACLQMAIHSLSGNESTVLLA 120			
DB	65 PWTFLMLATLTDVLSSSTQPKMALIFVHFKIEYHACLQVFFIHAFSSVSGVLT 124			
OY	121 MAFDFVYVACIPLHRAVYLTLPVTKIGVAAVVGAAALPVPFVKOLPQRSNLSHS 180			
DB	125 MALDRIYVACIPLHRSSTILTSVATIKLGVAVVRGLVSPFCFNVSRMPFCNKIIP 184			
OY	181 YCIHDDYKLCADDIRVNVVGLIYISAIGLDSLISFYLLIKTVGL-TREAQAKA 239			
DB	185 YCEHNAVYKIVCADIRVNRNGYGLFAFVYGGDIYISVYMWILRAYLRPSGEARLKA 244			
OY	240 FGTCSVHCANVFIFVVPFGLSMVHRESRRDSPLEVILANTIIYLLVPPVLANPIYGVKTK 299			
DB	245 FGTCSHSGVILITLIPALFTPLTFRHGHVPRVVAHMFANVYLLVPPMLNPIYGVRTK 304			
OY	300 EIKRILRLFLHY 311			
DB	305 QIRDRYTRGFCY 316			
RESULT 15				
ID	09EQ07	PRELIMINARY;	PRT;	319 AA.
AC	09EQ07;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DE	MOR 3/Beta4 (Olfactory receptor MOR1-1).			
OS	Mus musculus (Mouse).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RM	[1]			

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RP SEQUENCE FROM N.A.
RC STRAIN-129SV.
RX MEDLINE-20570519; Pubmed-11121057;
RA Bulger M., Bender M.A., van Doorninck J.H., Wertman B., Farrell C.M.,
RA Felsenfeld G., Groudine M., Hardison R.;
RT "Comparative structural and functional analysis of the olfactory
RT receptor genes flanking the human and mouse beta -globin gene
RT clusters";
RN Proc. Natl. Acad. Sci. U.S.A. 97:14560-14565(2000).
RP
RP SEQUENCE FROM N.A.
RA Zhang X., Firestein S.J.;
RT "The olfactory receptor gene superfamily of the mouse.";
RN Nat. Neurosci. 0:0(2002).
RP
RP [3]
RP SEQUENCE FROM N.A.
RP Adams M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF133300; AAG1684.1; -
DR EMBL; AY072988; AAL60651.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRHDOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECIP_FL_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECIP_FL_2; 1.
RM Receptor.
SQ SEQUENCE 319 AA; 35979 MW; 87FC0385FD19050A CRC64;
Query Match 52.8%; Score 856.5; DB 11; Length 319;
Matches 165; Conservative 53; Mismatches 89; Indels 1; Gaps 1;
QY 2 WVDPNGNESSATYFLLIGLPGLEAEQWLAFFLCSLYLVAIVGNTIIVYVTEHSLHP 61
Db 1 MATSNSTISTSTFELTITPGYEEFHMHHSIFPCFLYLAVGICGMIMLIHYTDRLEHP 60
QY 62 MYIFLCMISGDIILISTSMRKMALIFWNSNTTIOFDACILQMAFIAHISLGMESTVILAM 121
Db 61 MYIFLAMLSITDMAASLPTMSLFVNLWSISKEIOFNICVOMFLHTFSFESSVILAM 120
QY 122 AFDRTVAICHPLHAHTVTLFPRVTIGVAVAVRGAALAAFLVFEFKOLPFCRSNITLSHY 181
Db 121 ALDRVVAICHPLRATVITLIPKLIANIGTAAIIRSSILITPLARLAFFPGCSVILSHSY 180
QY 182 CLHODVAKLACDDIVANNVYGLVYIISAIGDSLISLSTYLLIKTVGL-TRDAQAAAF 240
Db 181 CLHODMIRIACADIDFNNTIYGLVTLTLMGMDSLGIFVSYVYLHSHVAKISREGRLRAL 240
QY 241 GCVSVHCAVVEFFYVPIGLSWVHRFSKRROSLPVIILANITVLLPVLNPLIVYGVKTRK 300
Db 241 NTCASHICAVLILYVPMIGLSIVHRAKHSPLIHIFAAHITLVLPVPLNPLIIVSVKIKQ 300
QY 301 IRORIILRL 308
Db 301 IREGIILHL 308

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Search completed: March 26, 2003, 09:55:37  
Job time : 89 secs